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(71) Applicant *(for all designated States except US)*: **EMORY UNIVERSITY** [US/US]; 401 Administration Building, Atlanta, GA 30322 (US).

(72) Inventor; and
(75) Inventor/Applicant *(for US only)*: **DEVINE, Scott, E.** [US/US]; 1107 Dan Johnson Road, N.E., Atlanta, GA 30307 (US).

(74) Agent: **MEIKLEJOHN, Anita, L.**; Fish & Richardson P.C., 225 Franklin Street, Boston, MA 02110-2804 (US).

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(54) Title: COMPOSITIONS AND METHODS FOR IDENTIFYING ANTIVIRAL AGENTS

(57) Abstract: Disclosed are compositions and methods that can be used to identify antiviral compounds. The methods can be carried out by exposing a cell that expresses a host factor to a candidate compound. If the expression or activity of the host factor, which is a protein we identified by virtue of its influence on the endogenous retrovirus-like Tyl element in yeast, is inhibited, the candidate compound is a potential antiviral agent. Such agents can be further tested, if desired, by determining whether they inhibit the ability of the virus to infect a cell or replicate within it.

COMPOSITIONS AND METHODS FOR IDENTIFYING ANTIVIRAL AGENTS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of the priority date of U.S. Provisional Application No. 60/378,711, which was filed on May 7, 2002. For the purpose of any national phase application that is subsequently prosecuted in the United States, the entire content of the provisional application is incorporated herein by reference.

TECHNICAL FIELD

This invention relates to compositions and methods for identifying antiviral agents, including those that are effective against retroviruses, such as human immunodeficiency viruses.

BACKGROUND

Retroviruses cause diseases such as acquired immune deficiency syndrome (AIDS), and they also play a causative role in cancer. Retroviruses generally encode Gag and Pol as well as additional proteins that are required to carry out their life cycles. These life cycles are complex, and they include (1) the assembly of virus particles (2) reverse transcription of mRNA and (3) integration of cDNA into the genome. Given the increasing prevalence of retroviral diseases, there is a need for new anti-viral strategies and treatments for retroviral diseases. There is also a need for new methods to identify such antiviral compounds and treatments.

SUMMARY OF THE INVENTION

The present invention is based, in part, on studies that exploited a collection of gene deletion mutants to identify proteins in yeast cells that influence the endogenous retrovirus-like Ty1 element (these proteins are referred to below as "host factors"). As described further below, Ty1 is a retrotransposon (sometimes called a retroposon) present in yeast, that is related to retroviruses; Tyl uses a mechanism similar to that used by retroviruses to integrate into the genome of a host cell. In our studies, we identified 105 yeast genes and the sequences of human proteins that are homologous to the host factors encoded by many of these yeast genes. At least 27 of the yeast host factors had significant homology to human proteins (with BLAST Expect values of $<10^{-30}$). The Ty1 host factors identified in yeast can

be used to study Ty1 and identify antiviral agents. Homologous proteins in higher organisms, such as the human homologs shown in Figure 4, can also be used to identify antiviral agents. Accordingly, the present invention features methods of screening agents for antiretroviral activity and compositions useful in such screens (*e.g.*, collections of host factors and cells in which one or more host factors have been inactivated). As described further below, the screening methods can be designed to detect a change (*e.g.*, a decrease) in the expression or activity of a host factor. Expression can be detected by any of the methods presently known in the art (*e.g.*, Northern blot assays, RT-PCR or other PCR-based amplification assays, RNAse protection assays, or in antibody-based assays (where the expression measured is protein expression, rather than gene expression), *etc.*; expression can also be examined in microarrays). Activity can similarly be measured by known assays and techniques (*e.g.*, kinase assays, cellular proliferation assays, *etc.*).

As used herein, a "host factor" is a yeast protein encoded by a gene identified in Table 1, a human homolog thereof (including those shown in Figure 4), a homologous protein in another animal, or a fragment, other mutant (*e.g.* a substitution mutant), or derivative (*e.g.*, a protein encoded by a splice variant or a protein to which additional amino acids residues have been attached) of any of these proteins. Where the host factor is not naturally occurring, it must retain one or more of the biological activities of the corresponding wild type host factor or it must function in the methods described herein. Homologous proteins (*e.g.* a mouse homolog or a homolog from a non-human primate) and fragments, other mutants, and derivatives of host proteins can be identified by their ability to function in a manner that is substantially equivalent to the yeast and human host factors described herein. A given protein will function in a manner that is substantially equivalent to that of a yeast or human host factor described herein if it exhibits one or more of the known, natural functions of the host factors (see Figure 5) or if it works in one or more of the screening assays set forth below. For example, a protein that constitutes a fragment of the protein encoded by *ARD1* or a fragment of SEQ ID NO:16 (a human homolog of the protein encoded by *ARD1*) is a host factor so long as it can be used in place of (*i.e.*, can effectively substitute for) the protein naturally encoded by *ARD1* or the protein represented by SEQ ID NO:16 in one of the assays described herein for identifying antiviral agents. This is not to say that the homologous, mutant, or variant protein need exhibit activity as robust as that of

its wildtype counterpart. Retention of even a small amount of the activity is sufficient so long as the homolog, mutant or variant protein is useful in detecting antiviral agents.

As illustrated further in the Examples below, Ard1/Nat1 encode a heterodimeric acetyltransferase. Together, these proteins modify target proteins, adding a chemical moiety to their N-termini. When working with the host factor Ard1, one could screen for compounds that bind to Ard1 or that inhibit the N-terminal acetylase activity using, for example, a substrate such as a histone. For example, one could monitor the incorporation of a radiolabeled acetyl group. Alternatively, one could assay for dimerization between Ard1 and Nat1 or for other known *in vivo* functions of Ard1 and/or Nat1. Such functions include teleomeric silencing and cell cycle progression (see Figure 5). Analogous assays can be used to test any of the factors for which a biological function or property (*e.g.* dimerization) is known or can be ascertained.

An "antiviral agent" is an agent that inhibits a virus in any therapeutically beneficial way (the antiviral agents identified using the compositions and methods described herein are expected to inhibit retroviruses (*e.g.*, those that infect humans and domesticated animals, such as cats) although the agents identified may have other therapeutic uses as well (*e.g.*, they may be useful in inhibiting viruses other than retroviruses)). For example, an antiviral agent can inhibit the ability of a retrovirus to infect cells, replicate within them, propagate, or infect secondary cells and can, as a consequence, improve a clinical sign or symptom in a patient who is infected with the retrovirus. The agent may also provide benefits to patients who have not yet been infected by reducing the likelihood that they will become infected following exposure to the retrovirus or that their symptoms will be as severe or prolonged as one would expect in the absence of treatment with the antiviral agent. Without limiting the invention to methods that identify anti-viral compounds having any particular features, in certain embodiments, candidate compounds can be identified as potential anti-viral agents by virtue of their ability to bind to or modify (*e.g.*, inhibit) the expression or activity of one or more of the host factors described herein. An antiviral compound can be a small molecule, an oligonucleotide (*e.g.*, an antisense oligonucleotide), an siRNA, an antibody (*e.g.*, a monoclonal antibody, a humanized antibody, a single chain antibody, or fragments thereof), or another type of protein or compound that can bind to and thereby inhibit the ability of a host factor to facilitate retroviral infection, replication, or propagation. For example, in the

event the host factor is a subunit of a larger protein complex (*e.g.*, a homodimer or heterodimer), the antiviral agent could, by virtue of binding to (or otherwise associating with) the host factor, prevent the host factor from participating in (or functioning in) the complex. The activities of many host factors are known in the art and representative examples are referenced in Figure 5.

Antiviral agents can be identified by carrying out the methods described herein in cells *in vivo* or *ex vivo*. The cell can be a yeast cell (*e.g.*, a *Saccharomyces* cell, such as *S. cerevisiae*), a bacterial cell (*e.g.*, *E. coli*), a mammalian cell (*e.g.* a human cell, such as a T lymphocyte), or a cell from an established cell line. Alternatively, one can employ cell-based assays, cell fractions, cell lysates, cell extracts, or *in vitro* assays with partially or substantially purified host factors. Regardless of the exact configuration of the assay, the antiviral agents can be identified in a two-step process: in the first step, one identifies a compound that binds to or that inhibits the expression or activity of a host factor, and in the second step, one tests the compound for antiviral activity. For example, in one embodiment, the invention features methods of identifying antiviral agents that include the steps of: (a) exposing a host factor to a candidate compound; (b) determining whether the candidate compound binds (*e.g.*, specifically binds) the host factor or inhibits the activity or expression of the host factor (a candidate compound that binds the host factor or inhibits the activity or expression of the host factor is a potential antiviral agent); (c) exposing a cell to the potential antiviral agent and a retrovirus; and (d) determining whether the potential antiviral agent inhibits the ability of the retrovirus to infect the cell, replicate therein, or exit the cell. A potential antiviral agent that inhibits the ability of the retrovirus to, for example, infect the cell, replicate therein, or exit the cell is an antiviral agent. The cell can be exposed to the potential antiviral agent before, during or after the cell is exposed to the retrovirus. Where the cell is a cell *in vivo*, one can determine whether a potential anti-viral agent is an antiviral agent by determining whether there is any improvement in a sign or symptom of the disease that is associated with the retroviral infection, or whether those signs and symptoms fail to appear as expected in the absence of administration of the antiviral agent.

The host factor can be partially or substantially pure (*e.g.* it can be separated from some or substantially all of the materials with which it is naturally associated; *e.g.*, 50, 60, 70, 75, 80, 85, 90, 95, 98, 99, or 100% pure) or in, for example, a cell fraction, lysate, or

extract. In these methods and other embodiments, in addition to determining, or as an alternative to determining, in step (b), whether the candidate compound binds (and, preferably, specifically binds) the host factor, one can determine whether the candidate compound inhibits the ability of the host factor to function. For example, one can determine whether the candidate compounds inhibit one or more of the activities of the host factor (again, some of these are noted in Table 2 and referenced further in Figure 5) or the host factor's expression.

As noted above, the methods of the invention can be carried out using intact or whole cells. Accordingly, the invention features methods for identifying an antiviral agent by: (a) exposing a first cell that expresses a host factor to a candidate compound; (b) determining whether the candidate compound binds to the host factor or inhibits the expression or activity of the host factor in the first cell (a candidate compound that inhibits the expression or activity of the host factor in the first cell is a potential antiviral agent); (c) exposing a second cell to the potential antiviral agent and a retrovirus; and (d) determining whether the potential antiviral compound inhibits the ability of the retrovirus to, for example, infect or replicate within the second cell. A potential antiviral compound that inhibits the ability of the retrovirus to infect or replicate within the second cell is an antiviral compound. As described further below, the first cell and the second cell (as referenced in any of the methods of the invention) may be of the same type or of different types and, if one desires, the first cell and the second cell may be the same cell.

The gene encoding a host factor can be deleted or inhibited in non-yeast cells (*e.g.*, a mammalian cell, such as a primary human cell or a cell from an established human cell line) by any method known in the art (*e.g.*, gene deletion or RNAi). That cell, or cells derived from the initial deletant cell, are within the scope of the present invention. Such cells (which can be isolated or placed in culture) can be used to determine whether the gene that was deleted (or otherwise inhibited) encodes a protein that facilitates retroviral infection or replication. It does so if, in its absence, a given retrovirus is less able to infect or replicate within the cell. Accordingly, the invention also features methods of determining whether a host factor is a promising target for a therapeutic agent. These methods can be carried out, for example, by exposing a cell in which one or more host factors have been silenced or impaired (by a knock out, other mutation, or antisense or RNAi procedure) to a retrovirus.

Such a cell is exposed to a retrovirus under conditions that would allow the retrovirus to infect the cell and carry out its life cycle. If the host factor is a promising target for a therapeutic agent, the retrovirus will not infect the cell or complete its life cycle as successfully as it otherwise would (control experiments using, for example, a corresponding wildtype cell, can be carried out). Any of the host factors described herein can be used in such an assay and any of the reagents suitable for use in the screening assay described above are suitable for use in identifying promising drug targets. For example, one can examine yeast or human host factors and either (or both in combination) can be studied in yeast or human cells. This method can be carried out before one screens for antiviral agents *per se*.

Preferably, the cell (be it the first, second, or only cell used) is one that is naturally infected by a retrovirus, but it can also be a cell that is rendered susceptible to infection (by, for example, being made to express appropriate receptors for the virus in question).

In the various embodiments of the invention, the host factor can be a yeast or human host factor or, where more than one factor is present, a combination thereof. Alternatively, the host factor can be a homologous protein from another species or, as described above, a fragment, other mutant, or variant of any of these proteins. The factor(s) can be naturally expressed by a cell employed in the assays described herein or they can be expressed following transfection with an appropriate nucleic acid sequence (optionally, under the control of a constitutively active or inducible promoter and/or other regulatory elements). Cells that have been genetically modified to express a host factor are also within the scope of the invention. The nucleic acid sequence can also encode an affinity tag to facilitate purification or to confer some other desirable attribute. In the event the host factor is a human host factor, it can include the sequence of any of SEQ ID NOs:5-501.

Kits containing reagents to carry out the methods of the invention and those reagents *per se* are also within the scope of the present invention. For example, the invention features collections of the host factors described herein (yeast and human) and nucleic acid sequences encoding them. For example, the invention features a kit that includes the yeast host factor Ard1 and/or Nat1, Sin3, or Spt4, or one or more of the corresponding human homologs and one or more of the reagents necessary for determining whether the host factor(s) included retain their biological activity in the presence of a candidate anti-retroviral agent (*e.g.*, a protein substrate to assess acetyltransferase or deacetylase activity). The same kit could

include the DNA repair protein Rad52 and reagents that could be used to examine the ability of this host factor or a homologue or derivative thereof, to mediate homologous recombination in the presence of a candidate antiviral agent. Alternatively, or in addition, the kit can contain a host factor that influences protein folding or otherwise modifies cellular proteins (*e.g.*, kinases and proteases) and reagents for assaying these biological activities. These descriptions exemplify the kits of the invention. Others may contain any combination of the yeast or human host factors we identified (the yeast host factors are shown in Tables 1 and 2 and the human homologues are shown in Figure 4). The factors, or cells that express them, and reagents to assay their expression or activity (*i.e.*, an activity set out in Table 2 or Figure 5) in the presence of candidate antiviral agents, can be packaged with instructions for use (which may be written or contained in some other medium).

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B illustrate events relevant to the functional genomic screen we used to identify genes that affect Ty1. Fig. 1A is a schematic of the test Ty1 plasmid pAR100 (a composition within the scope of the invention), which was introduced into each of the 4,483 *S. cerevisiae* deletion strains tested.

The results obtained in an exemplary screen on synthetic complete medium lacking histidine are shown in the photograph of Fig. 1B. Four knockout strains (listed to the right of the plate) were tested in triplicate (listed 1-3 above the plate) on each plate (after inducing retrotransposition). Two controls were included on each plate. The negative control was the wildtype 4743 strain (Winzeler *et al.*, *Science* <u>285</u>:901-906, 1999) carrying the pRS316 plasmid (Sikorski and Hieter, *Genetics* <u>122</u>:19-27, 1989; lower left), and the positive control was the wildtype 4743 strain carrying the pAR100 Ty1 test plasmid (lower right). The positive control yielded a retrotransposition rate of approximately 1% under our test conditions, as judged by the appearance of His^+ cells. The YMR032w strain (plated in the third row from the top) showed a clear decrease in Ty1 retrotransposition (in triplicate), and

all three patches showed decreased numbers of His^+ cells. An additional 24 plates were used to test each box of 96 deletion strains.

Figures 2A–2C represent transposition data for the chromatin mutants. The photographs in Fig. 2A show the results obtained when the ten chromatin mutants identified in our screen were tested. On each plate, the top row shows retrotransposition data from the original three transformants, the second row from the top shows retrotransposition in cells from the frozen stocks of those original three transformants, and the third row shows retrotransposition in cells of the three re-transformants. Negative and positive controls are shown at the bottom of each plate as described for Figure 1B. Equivalent results were obtained with knockout strains that were independently generated using a *LEU2* deletion cassette to delete the same genes in the 4741 strain background. The photograph of Fig. 2B illustrates a quantitative retrotransposition assay. Cells were scraped from the SC plus 5-Foa plate, diluted to an OD_{600} of 1.0, and 2-fold serial dilutions were plated from left to right. Fig. 2C lists the fold changes for the chromatin mutants that were determined using the dilution assay depicted in Fig. 2B. Each mutant was tested in triplicate and the value shown represents the average of the three estimates. The fold-change estimates for all of the mutants in Table 1 were obtained. Fifty of the mutants yielded 3-8-fold changes and 51 yielded greater than 8-fold changes.

Figure 3 is an illustration of the Ty1 retrotransposition cycle. The cycle begins with the transcription of Ty1 elements in the nucleus (step 1). Ty1 mRNAs are produced and exported to the cytoplasm (steps 2 and 3). The mRNAs are next translated to produce Ty1 Gag and Pol proteins (step 4). Ty1 virus-like particles are assembled and Ty1 mRNAs are packaged into these particles (step 5). The arrows exiting and entering the cell indicate the point at which retroviruses with envelope (ENV) genes can exit a cell and infect a new cell. The Ty1 mRNAs next are copied into double stranded (ds) cDNAs using reverse transcriptase (step 6). The cDNAs and Ty1 integrase (IN) then are imported back into the nucleus (step 7). The cDNAs finally are integrated into chromosomal DNA (step 8).

Figure 4 is a compilation of human proteins homologous to the yeast host factors identified in the studies described below (the human host factors are represented by SEQ ID NOs:5-501). The GenBank™ accession number is provided for each sequence. The human proteins were identified by using the sequences of the yeast host factors as queries in a

BLAST search of databases available through the National Center for Biotechnology Information (NCBI). Human homologs or homologs from other species can be identified using this resource. For example, one can identify homologs using the default parameters set by the search program (BLOSUM62 is the matrix; word length 3; gap penalty 11; gap extension penalty 1). Alternatively, one can accept matches under less stringent circumstances. Physical assays can also be performed to identify homologous sequences. For example, one can probe a cDNA library with a sequence that encodes one or more of the yeast or human host factors identified herein so that the sequence, which acts as a probe, hybridizes with potential target sequences in the library under conditions of high stringency. Highly homologous sequences will remain base-paired even following washing under conditions of high stringency (*see* the conditions of high stringency in Sambrook *et al.*, *Molecular Cloning – A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

Figure 5 is a Table summarizing the functions of host factors. These functions are among those that can be assessed when determining whether a candidate compound inhibits the activity of a host factor.

DETAILED DESCRIPTION

Ty1 is an LTR (long terminal repeat) retrotransposon in yeast that is a relative of vertebrate retroviruses (Boeke *et al.*, *The Molecular and Cellular Biology of Yeast Saccharomyces: Genome Dynamics, Protein Synthesis, and Energetics*, J.R. Broach *et al.* Eds, pp 193-261, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y, 1991). Like retroviruses, Ty1 encodes homologs of Gag and Pol proteins, forms virus-like particles, and transposes through an RNA intermediate using reverse transcriptase (Boeke *et al.*, *supra*). Ty1 has a complex retrotransposition cycle that begins in the nucleus with the transcription of full-length Ty1 elements. As the cycle progresses, virus-like particles are assembled in the cytoplasm and, ultimately, double-stranded Ty1 cDNAs are generated from Ty1 mRNAs. The cycle is completed when these newly synthesized cDNAs integrate into chromosomal DNA in the nucleus of the host cell. Since the transposition cycle is complex and spans several intracellular compartments, it is likely to involve a wide range of host factors.

The human genome project has revealed that transposable genetic elements are abundant in the genomes of model organisms and humans. We have used bioinformatic, genomic, and biochemical tools to study the phenotypic effects of these transposons on the genomes of yeast and humans. Our work with the Ty1 retrotransposon of yeast has revealed that this transposon integrates very non-randomly in the yeast genome. Ty1 usually avoids integrating into the protein coding, gene-rich regions of the genome, and instead inserts preferentially upstream of tRNA genes and other genes that are transcribed by RNA polymerase III. Although this targeting system generally protects yeast genes from undesired transposon mutations, Ty1 does occasionally integrate into genes and cause mutations. To understand this targeting system better, we have conducted a functional genomics screen for factors that affect Ty1 transposition using the recently completed gene deletion collection generated by the Saccharomyces Deletion Project. We identified a number of cellular factors that influence Ty1. Our preliminary results indicate that transposon insertion polymorphisms (TIPS) and other types of Deletion/Insertion Polymorphisms (DIPs) represent a major source of genetic diversity in humans.

As noted, we identified host factors that influence Ty1 (and therefore function to facilitate Ty1 transposition) by screening the collection of mutants generated by the Saccharomyces Genome Deletion Project (Winzeler *et al.*, *Science* 285:901-906, 1999). An advantage of this approach is that all ~6,200 yeast genes have been deleted in this single isogenic collection of knockout strains, allowing many genes to be tested in parallel for possible effects on a given process (in this case, Ty1 retrotransposition). Approximately 17% of the genes in yeast are "essential" and therefore produce lethal phenotypes upon gene deletion (Winzeler *et al.*, *Science* 285:901-906, 1999). However, the remaining ~83% of gene knockouts are viable and can, therefore, be tested readily for additional phenotypes.

Just over 100 genes (105) that influence many different aspects of the Ty1 retrotransposition cycle were identified from uor analysis of 4,483 homozygous diploid deletion strains. Of these mutants, 46 had significantly altered levels of Ty1 cDNA. Thus, approximately half of the mutants apparently affected the early stages of retrotransposition leading up to the assembly of virus-like particles and cDNA replication, whereas the remaining half effected steps that occur after cDNA replication. Thus, if one specifically wished to identify an antiviral agent that acted by inhibiting either the early stages of the viral

life or the later stages of the viral life cycle, the assays of the invention could be configured to assay the expression or activity of host factors affected at either of these relative times. Although most of the mutants retained the ability to target Ty1 integration to tRNA genes, two mutants had reduced levels of tRNA gene targeting. Thus, should one wish to search for antiviral agents that specifically interfered with gene targeting, the assay could be configured to assess the expression and/or activity of one of these two host factors.

As illustrated in Fig. 1A, we induced retrotransposition by growing cells carrying the test plasmid in a galactose-positive environment, and then assayed transposition by replicating to media lacking histidine. The test plasmid carries Ty1 and *HIS3* sequences under the control of a Gal1 promoter. Because the deletion mutants lack an ability to grow in histidine, we were able to identify the genes that encode proteins required for retrotransposition by examining the ability of each of the mutant strains of yeast, carrying the test plasmid, to survive on histidine-free culture medium. If Ty1 integrates into the yeast genome, as evidenced by the cell's ability to survive on the histidine-free medium, we can conclude that the protein that is absent from the host deletion mutant is not one required for the retrotransposition. To the contrary, if the protein that is absent is required for retrotransposition, the yeast cells will not grow or will grow much less well. If there is no retrotransposition (because a protein required for that event has been effectively deleted from the mutant yeast cell), the cell will not express the exogenous *HIS3* sequence and, consequently, will not be able to survive, or will have an impaired ability to survive, when plated on histidine-free medium. The assay also can detect deletions that cause increases in transposition by detecting increased numbers of HIS-positive cells on media lacking histidine.

The results we obtained represent a dramatic increase in the number of host factors that are known to affect Ty1 and provide information on the relationship between Ty1 and its yeast host. In addition, we discovered that many of the yeast host factors are homologous to human proteins, and we describe how factors from either or both sets can be used to identify antiviral agents (of course, homologs from other animals, such as rats, mice, or other rodents, rabbits, cats, dogs, sheep, cows, horses, goats, pigs, and non-human primates can be used in these methods as well).

The 105 genes that were identified in the initial study with *Saccharomyces* mutants are shown in Table 1.

Table 1. Deletion strains with moderate or strong changes in Ty1 retrotransposition (retrotransposition levels measured in triplicate with dilution assays)

Group (no. of genes)	*Gene Deleted* (fold-change in retrotransposition (average of three measurements))
Chromatin (10)	ARD1 (-20.0); NAT1 (-32.0); SAP30 (-32.0); SIN1 (SPT2; -16.0); SIN3 (-16.0); SIN4 (-32.0); SPT4 (-32.0); SPT10 (-4.0); SPT21 (-16.0); STB5 (-32.0)
Chromatin Remodeling (4)	SNF2 (~ -10.0); SNF5 (~ -10.0); SNF6 (~ -10.0); SWI3 (~ -10.0)
DNA Repair (4)	APN1 (-9.3); MMS22 (-6.0); RAD52 (-4.0); XRS2 (-4.0)
Miscellaneous (27)	APG17 (-10.7); APL5 (-16.0); BEM1 (-8.0); BUD6 (-4.0); CHO2 (-4.0); CYK3 (-16.0); DCC1 (-12.0); ERV14 (-5.3); FYV3 (-16.0); HOF1 (CYK2; -16.0); JNM1 (-3.3); KCS1 (-6.7); KRE24 (-4.0); MAD2 (-3.3); MFT1 (-8.0); PAT1 (-16.0); NUM1 (-8.0); SCP160 (-4.0); SDF1 (-3.3); SEC22 (-9.3); SEC65 (+3.3); SMI1 (-8.0); SWA2 (-4.0); TPM1 (-8.0); TPS2 (-8.0); VPH1 (-8.0); VPS9 (-4.0)
Nuclear Transport (2)	NUP84 (-12.0); NUP133 (-5.3)
Protein Folding /Modification (8)	CPR7 (-3.3); DBF2 (-8.0); DOA4 (-8.0); MCK1 (-32.0); NAT3 (-26.7); PFD1 (-4.6); SSE1 (-21.3); TCI1 (-3.3)
Ribosomes/Translation (9)	DBP3 (-8.0); RPL6A (-16.0); RPL14A (-8.0); RPL16B (-4.6); RPL19B (-13.3); RPL20B (-10.7); RPL21B (-6.7); RPP1A (-8.7); RPS10A (-10.7)
RNA Metabolism (8)	CBC2 (-24.0); DBR1 (-13.3); LEA1 (-16.0); LSM1 (-32.0); NOP12 (-13.3); RIT1 (-24.0); STO1 (CBC1; -32.0), YDL033c (-8.0)
Transcription (10)	CTK1 (-12.0); DEP1 (-37.3); HAC1 (-4.0); PHO23 (-6.0); POP2 (-13.3); RPA49 (-16.0); RTF1 (-9.3); SRB8 (-8.7); SSN2 (-8.0); SUB1 (-7.3)
Transcription/ elongation (7)	ELP2 (-6.0); ELP3 (-10.7); ELP4 (-6.0); ELP6 (-13.3); IKI3 (ELP1; -10.7); KTI12 (-4.0); THP2 (-6.0)

Unknown (16)	YBR077c (-6.0); YDL115c (-12.0); YDR496c (-10.7); YFL032w (-3.3); YGL250w (-5.3); YGR064w (-16.0); YKL053c-A (-4.0); YLR052w (-3.3); YLR322w (-8.7); YML010c-B (-16.0); YNL226w (-16.0); YNL228w (-16.0); YNL295w (-3.3); YOL159c (+4.0); YOR292c (-10.7); YPL080c (-4.7)

At least 39 of the 105 factors have significant homology to human proteins (with BLASTp Expect values of < 10^{-13}; Table 2). This is not to say that human proteins that exhibit less homology with the yeast host factors are excluded from the invention or are less useful in the methods described herein. The yeast host factors, their human homologs, or homologous proteins similarly identified in other species (*e.g.*, identified by searching sequence databases, using the identified yeast or human sequences as queries) can be used to screen compounds that affect (*e.g.*, inhibit in any therapeutically useful way) human retroviruses such as HIV (e.g., HIV-1 or HIV-2 of any subtype or clade). Such antiviral agents could, of course, prove effective in treating or preventing diseases associated with retroviruses (*e.g.*, acquired immunodeficiency syndrome (AIDS).

Table 2. Ty1 host factors with significant matches to human host factors.

Yeast Protein	Human BLAST Score	Function/Phenotype
Chromatin (4)		
Ard1	2e-38	N-terminal acetyltransferase
Nat1	1e-75	N-terminal acetyltransferase
Sin3	5e-68	Histone deacetylation
Spt4	2e-17	Chromatin factor
DNA Repair (1)		
Rad52	3e-38	Homologous recombination
Miscellaneous (9)		
Apl5	5e-92	Vesicular trafficking
Erv14	4e-17	Localized to ER-derived vesicles
Kcs1	9e-23	Inositol hexakisphosphate kinase 3
Mad2	8e-37	Mitotic arrest deficient
Scp160	2e-33	High density lipoprotein binding protein
Sdf1	3e-26	Sporulation deficient
Sec22	1e-28	Vesicular trafficking
Vph1	1e-169	Proton pump in clatherin vesicles
Vps9	2e-20	Rab5 GDP/GTP exchange factor

Protein Folding/Modification (6)		
Cpr7	3e-39	Cyclophilin D
Dbf2	4e-56	Serine/threonine kinase
Doa4	5e-47	Ubiquitin specific protease 8
Mck1	2e-69	Protein kinase
Nat3	5e-28	N-terminal acetyltransferase
Sse1	1e-120	Hsp70 family
Ribosomes/Translation (7)		
Dbp3	2e-73	RNA helicase
Rpl6a	4e-28	Ribosomal protein 6
Rpl16b	8e-51	Ribosomal protein 13a
Rpl19b	3e-34	Ribosomal protein 19b
Rpl20b	3e-42	Ribosomal protein 18a
Rpl21b	8e-40	Ribosomal protein 21
Rps10a	1e-24	Ribosomal protein S10
RNA Metabolism (5)		
Cbc2	2e-35	Nuclear cap binding protein subunit 2
Dbr1	4e-66	RNA lariat debranching enzyme
Lsm1	2e-17	Lsm1 protein
Sto1/Cbc1	6e-13	Nuclear cap binding protein subunit 1
Ydl033c	6e-41	5-methylaminomethyl-2-thiouridylate-methyltranferase
Transcription (2)		
Ctk1	1e-69	Ctk1 kinase
Pop2	2e-49	CCR4 complex
Transcription Elongation (4)		
Elp2	3e-80	Transcription elongation/Apoptosis inhibitor
Elp3	0	Histone acetyltransferase
Iki1 (Elp1)	4e-74	RNA Polymerase II elongator subunit
Kti12	9e-15	RNA Polymerase II elongator associated
	protein	
Unknown (1)		
Ydr496c	1e-38	Unknown

Human protein sequences homologous to the yeast host factors we identified initially are shown in Figure 4. The sequences were identified by a conventional protein Blast™ search. These proteins and other host factors (as defined above) can be used to identify antiviral agents.

For example, antiviral agents can be identified by, first, identifying a compound that binds to or that inhibits the expression or activity of a host factor and, second, testing the

compound for antiviral activity. For example, the method can be carried out by (a) exposing a host factor (or a number of host factors) to a candidate compound; (b) determining whether the candidate compound binds the host factors or inhibits the activity or expression of the host factors (a candidate compound that binds the host factors or inhibits the activity or expression of the host factors is a potential antiviral agent); (c) exposing a cell to the potential antiviral agent and a retrovirus; and (d) determining whether the potential antiviral agent inhibits the ability of the retrovirus to, for example, infect the cell, replicate therein, or exit the cell. A potential antiviral agent that inhibits the ability of the retrovirus to infect the cell or replicate therein (or that otherwise lessens the detrimental effect of a retroviral-associated disease on a patient) is an antiviral agent.

The candidate compound can be essentially any type of chemical or biological entity, and those of ordinary skill in the art will be able to identify sources of compounds to be tested in the methods described herein. There have been recent advances in high throughput screening, and those advances have given rise to a need for large numbers of compounds. Those of ordinary skill in the art routinely acquire and screen thousands of compounds in search of useful therapeutic agents. Compound libraries can be generated or obtained from a commercial supplier. For example, LeadQuest®, a library containing more than 80,000 compounds, can be obtained from Tripos (St. Louis, MO). Standard or custom made libraries can also be obtained from, for example, *Ab Initio* PharmaSciences (Basel, Switzerland), Affymax Research Institute (Santa Clara, CA), Array BioPharma, Inc. (Boulder, CO), Ascot Fine Chemical (Cambridge, England), ASDI Biosciences (Newark, DE), BioLeads GmbH (Heidelberg, Germany), and BIOMOL Research Laboratories, Inc. (Plymouth Meeting, PA). The compounds may be chiral compounds, small heterocycle motifs, peptidomimetics, or natural product derivatives.

When in the form of a library, the library can be a biological library (of, for example, peptides, oligonucleotides, or antibodies) or a spatially addressable parallel solid phase or solution phase library. Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (*Proc. Natl. Acad. Sci. USA* 90:6909,1993); Erb *et al.* (*Proc. Natl. Acad. Sci. USA* 91:11422, 1994); Zuckermann *et al.* (*J. Med. Chem.* 37:2678, 1994); Cho *et al.* (*Science* 261:1303, 1993); Carrell *et al.* (*Angew. Chem. Int. Ed.*

Engl. 33:2059, 1994); Carell *et al.* (*Angew. Chem. Int. Ed. Engl.* 33:2061, 1994); and Gallop *et al.* (*J. Med. Chem.* 37:1233, 1994).

Libraries of compounds may be presented in solution (*e.g.*, Houghten, *Bio/Techniques* 13:412-421, 1992), or on beads (Lam, *Nature* 354:82-84, 1992), chips (Fodor, *Nature* 364:555-556, 1993), bacteria (U.S. Patent No. 5,223,409), spores (Patent Nos. 5,571,698; 5,403,484; and 5,223,409), plasmids (Cull *et al. Proc. Natl. Acad. Sci. USA* 89:1865-1869, 1992) or on phage (Scott and Smith, *Science* 249:386-390, 1990; Devlin, *Science* 249:404-406, 1990; Cwirla *et al.*, *Proc. Natl. Acad. Sci. USA* 87:6378-6382, 1990; and Felici, *J. Mol. Biol.* 222:301-310, 1991).

Where inhibitors of gene expression are assayed, the inhibitor can be an antisense oligonucleotide or a sequence suitable for use in RNAi (e.g., a dsRNA, siRNA, or miRNA). RNAi (RNA interference) refers to the process of introducing a homologous double stranded RNA (dsRNA) into a cell to specifically target a gene sequence, resulting in null or hypomorphic phenotypes. RNAi is interesting because it is generally carried out with a double stranded molecule, rather than single-stranded antisense RNA; it is highly specific; it is remarkably potent (only a few dsRNA molecules per cell may be required for effective interference); and the interfering activity (and presumably the dsRNA) can cause interference in cells and tissues far removed from the site of introduction.

Antisense oligonucleotides can also be tested as antiviral agents according to the methods of the invention and are well known in the art. Nucleic acids that hybridize to a sense strand (*i.e.*, a nucleic acid sequence that encodes protein, *e.g.*, the coding strand of a double-stranded cDNA molecule) or to an mRNA sequence are referred to as antisense oligonucleotides. While antisense oligonucleotides are "antisense" to the coding strand, they need not bind to a coding sequence; they can also bind to a noncoding region (*e.g.*, the 5' or 3' untranslated region). For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of an mRNA (*e.g.*, between the -10 and +10 regions of a target gene of interest or in or around the polyadenylation signal). Moreover, gene expression can be inhibited by targeting nucleotide sequences complementary to regulatory regions (*e.g.*, promoters and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells (see generally, Helene, *Anticancer Drug Des.* 6:569-84, 1991; Helene, *Ann. N.Y. Acad. Sci.* 660:27-36, 1992; and Maher, *Bioassays*

14:807-15, 1992). The sequences that can be targeted successfully in this manner can be increased by creating a so-called "switchback" nucleic acid. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines on one strand of a duplex. Fragments having as few as 9-10 nucleotides (*e.g.*, 12-14, 15-17, 18-20, 21-23, or 24-27 nucleotides) can be useful in the screening methods described herein.

Methods known in the art can also be used to determine whether a compound binds (*e.g.*, specifically binds) a host factor or the gene that encodes it. Similarly, methods known in the art can be used to determine whether a compound inhibits one or more of the activities of the host factor. Some of the functions that can be examined, and the methods by which they may be assessed, are summarized in the Table shown as Figure 5.

EXAMPLES

Construction of the test Ty1 plasmid, pAR100

A *Bam HI/Not* I fragment carrying a Gal-Ty1-neo insert (Devine and Boeke, *Genes Dev.* 10:620-633, 1996) was cloned into the *Bam H* I and *Not* I sites of the pRS316 plasmid (Sikorski and Hieter *Genetics* 122:19-27, 1989) to generate the plasmid p3.1. A PCR cassette carrying the *HIS3* gene then was inserted into p3.1 at bases 6,168 to 7,080 of the Gal-Ty1-neo insert in both the forward and reverse orientations by homologous recombination in yeast (Kaiser *et al. Methods in Yeast Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1994). The HIS3 cassettes were generated by PCR using the pRS403 plasmid (Sikorski and Hieter *Genetics* 122:19-27, 1989) as a template and oligonucleotide primers with the following sequences:

(SD516) 5'-TTACATTGCACAAGATAAAAATATATCATCATGAACAATAAA ACTAGATTGTACTGAGAGTGCAC-3' (SEQ ID NO:1),

(SD517) 5'-CGCCGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGTTACA ACCCTGTCGGGTATTTCACACCG-3' (SEQ ID NO:2),

(SD518) 5'-TACATTGCACAAGATAAAAATATATCATCATGAACAATAAAAC TCTGTCGGGTATTTCACACCG-3' (SEQ ID NO:3), and

(SD519) 5'-CGCCGTCCCGTCAAGTCAGCGTAATGCTCTGCCAGTGTTACAA CCAGATTGTACTGAGAGTGCAC-3' (SEQ ID NO:4).

The neo gene of Gal-Ty1-neo was replaced by the *HIS3* gene using this strategy. Transposition levels were similar for both constructs, and the reverse orientation construct, pAR100, was chosen for the screen (Figure 1A).

The Ty1 transposition assay

The complete set of homozygous gene deletion strains (release 2) was obtained from Research Genetics (Huntsville, AL). A complete list of the genes tested can be viewed at the Research Genetics website. These deletion strains were transformed with the pAR100 test plasmid in batches of 96 following the order established by the Saccharomyces Genome Deletion Project using a lithium acetate method adapted to 96-well culture boxes (Winzeler *et al., Science* 285:901-906, 1999). All media were prepared as outlined previously (Kaiser *et al. Methods in Yeast Genetics*, Cold Spring Harbor.Laboratory Press, Cold Spring Harbor, N.Y., 1994). Transformation reactions were plated on synthetic complete (SC) minus uracil (SC-U) medium and three independent transformants were patched onto SC-U medium. These plates were replica-plated to medium containing SC-U plus 2% galactose and incubated for four days at room temperature (24°C) to induce transposition. They also were replica-plated to yeast peptone glycerol (YPG) medium to identify strains that could not support respiration (these strains were eliminated from further analysis). The SC-U plus galactose plates then were replica plated sequentially to: i) SC-U plus glucose, ii) yeast peptone dextrose (YPD), iii) SC plus glucose containing 1.2 g/L 5-Fluoroorotic acid (5-Foa), and iv) SC minus histidine (SC-H) plus glucose (Figure 1B). Plates were incubated overnight at 30°C between each step.

Secondary Screens

All mutants that were positive in the initial screen were re-tested in a *GAL1*-lacZ reporter assay to identify host genes that influenced the *GAL1* promoter used to induce transposition from the Ty1 test plasmid. Only a small fraction of the mutant candidates affected the *GAL1* promoter as judged by the X-gal assay ((Kaiser *et al. Methods in Yeast Genetics*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1994), including deletions in several gal genes, and these were eliminated from further consideration. A second test was performed to determine whether the *HIS3* marker in the test Ty1 element was functioning in each putative Ty1 mutant. Host mutants that affected marker function would not be expected to yield a His^{+} phenotype after transposition and would be indistinguishable

from actual Ty1 mutants. Thus, we tested whether each mutant candidate (carrying a Ty1 test plasmid) could support a His$^+$ phenotype prior to the induction of transposition by replica-plating each strain to medium lacking histidine. A small number of strains were identified in this class, including strains carrying deletions in the known histidine biosynthesis genes (*his1*, *his2*, *his4*, *his5*, *his6* and *his7*), and these were removed from further consideration.

Dilution assays

Transposition levels were measured in triplicate for each mutant by plating serial dilutions of cells that had been induced for Ty1 transposition on medium that was selective for transposition events (SC-H) and on two control media (SC and SC-U). Cells were scraped from the SC plus 5-Foa patches into water and diluted to an OD_{600} of 1.0. Two-fold dilutions were prepared in 96-well microtiter dishes and then plated on all three media using a multichannel pipettor. The SC plate served as a control for adjusting the cells to an OD_{600} of 1.0, whereas the SC-U plate served as a control to ensure that the test plasmid had been eliminated successfully on the previous 5-Foa step. The number of cells growing at each dilution on the SC-H plate was compared to similar dilutions prepared from the wild-type strain and the fold-change was estimated (rounding to the nearest 2-fold dilution). The three independent measurements were averaged to produce the final fold-change value reported.

Targeting assays: The modified Ty1 element, placed under the control of the galactose-inducible *GAL1* promoter, was used to test retrotransposition as described previously (Devine and Boeke, *Genes. Dev.* 10:620-633, 1996; Boeke *et al.*, *Cell* 40:491-500, 1985). The yeast *HIS3* gene was engineered into this test Ty1 element as a convenient marker for retrotransposition events in the *his3Δ1* genetic background of the knockout collection (Winzeler *et al.*, *Science* 285:901-906, 1999). Thus, if Ty1 transposed from the test plasmid into the yeast genome, it carried with it the *HIS3* gene and conferred a His$^+$ phenotype to an otherwise His$^-$ strain (Figure 1).

Using this plasmid-based assay, deletion strains with significantly altered levels of Ty1 retrotransposition were identified readily from the knockout collection (Figure 1B). In fact, 2.3% of the yeast genes tested showed a Ty1 retrotransposition phenotype, for a total of 105 mutants in the collection of 4,483. The vast majority of the mutants had decreased levels of retro-transposition (only yml105c and yol159c had increased levels). Transposition mutants were independently confirmed by re-transforming each strain with the Ty1 plasmid

and re-testing it along with the original transformants and frozen stocks of the original transformants. The results of these comparisons were remarkably consistent (Figure 2A).

All of the mutant candidates identified in our initial screen were subjected to two secondary tests designed to eliminate host genes that affected our assay rather than Ty1 retrotransposition itself. As expected, gal and his mutants were identified in these secondary screens, along with a few other mutants. Although gal and his mutants represented unwanted byproducts of our genomic screen, these mutants were fully expected to affect our assay and thus served as excellent internal controls for the accounting system of the knockout collection. The remaining 105 Ty1 host factor (thf) mutants were considered to have actual Ty1 retrotransposition phenotypes. These mutants clustered into ten groups according to the known functions of the genes (Table 1). The data for the chromatin mutants are shown in Figure 2. Similar data were obtained for the remaining mutants in Table 1.

Although the patch assays alone indicated that the changes in retrotransposition levels generally were quite significant, quantitative retrotransposition assays also were performed on the mutants listed in Table 1. The results of these assays confirmed and extended the initial observations with the patch assays. Fifty of the mutants produced "moderate" (3- to 8-fold) changes in retrotransposition levels and fifty-one mutants produced "strong" (greater than 8-fold) changes in retrotransposition levels. An example of the assay is shown in Figures 2B and 2C. We also identified a number of mutants with "weak" (below 3-fold) changes in retrotransposition levels, and these strains were omitted from the collection of mutants.

Ty1 cDNA analysis: Ty1 cDNA was measured by Southern hybridization analysis after a 48-hour induction in medium containing galactose. DNA was isolated from duplicate pAR100 transformants and analyzed as follows. After measuring the DNA concentration of each sample with a spectrophotometer, 10 μg of DNA was digested with the restriction endonuclease *Afl* II (which cuts 2,472 bp from the right end of Ty1-*HIS3* cDNA) and run on a 1% agarose gel. The DNA was transferred to a nylon membrane (Osmonics) and then hybridized to a 1.4 kb probe that spanned the full *HIS3* gene. Using this strategy, cDNA originating from the pAR100 donor plasmid was detected, but cDNA arising from genomic Ty1 copies was not detected. The *HIS3* probe also hybridized to the linearized donor plasmid pAR100 and the *his3Δ1* allele in the BY4743 strain background, thereby generating

two additional bands in each lane (at 13 kb and 5 kb, respectively). These bands served as loading controls to ensure that equal amounts of DNA were analyzed in each lane. The prehybridization/ hybridization buffer contained: 6 X SSC, 0.01 M EDTA (pH 8.0), 5 X Denhardt's solution, 0.5% SDS, and 100 μg/ml sheared, denatured salmon sperm DNA. The prehybridization, hybridization, and final wash steps were carried out at 65°C. The washed membranes were exposed to XAR5 film, and also were analyzed with a Fujix BAS1000 phosphoimager after exposing the membranes to phosphoimaging screens. Ty1 cDNA was measured in the duplicate samples by digital analysis of the scanned images, and the duplicates were averaged to obtain the final values reported. The Ty1 cDNA levels were considered to be altered from wild-type if the average of the duplicate measurements was below 50%, or greater than 200%, of wild type control cDNA levels.

Identification of potential homologs:

We next performed BLAST searches (Altschul *et al.*, *J. Mol. Biol.* 215:403-410, 1990) to identify potential homologs of Ty1 host factors in other organisms. Full-length open reading frame translations were obtained for each of the genes listed in Table 1 from the Saccharomyces Genome Database and these sequences were used as BLAST queries against the non-redundant protein database at the National Center for Biotechnology Information (NCBI) using the default settings. Potential homologs were identified in a variety of organisms, including humans, with this approach, and the sequences of the human homologs are shown in Figure 4 (SEQ ID NOs:5-501). Using a BLAST Expect value cutoff of $<10^{-13}$, thirty-nine of the 105 genes listed in Table 1 encoded proteins with significant matches to potential human homologs (Table 2). Similar results were obtained for mouse and other organisms.

As will be evident from the studies described above, 105 genes that presumably influence many different aspects of the Ty1 retrotransposition cycle were identified from our analysis of 4,483 homozygous deletion strains. These genes are known to participate in a wide range of cellular processes, and we classified then into 11 major groups based on the known functions of the encoded proteins.

Forty-six of the mutants identified in our screen had altered levels of Ty1 cDNA as measured by Southern hybridization analysis (Table 3). Forty-four of these mutants had decreased levels of cDNA, whereas two mutants had increased levels of cDNA. Since we

eliminated mutants that affected the *GAL1* promoter used in our Gal-Ty1 donor plasmid, none of the mutants is expected to affect the initial transcription step of the retrotransposition cycle in this system. However, several subsequent steps of the cycle must be completed before any Ty1 cDNA can be replicated, and mutants with diminished levels of cDNA could be deficient in any of these steps. Such steps include: i) the initial processing of Ty1 mRNA in the nucleus, ii) the export of Ty1 mRNA from the nucleus, iii) the translation of Ty1 proteins on ribosomes, and iv) the assembly of virus-like particles in the cytoplasm. The cDNA levels might also be affected by changes in the rate of cDNA replication or turnover.

Nine of the ten chromatin mutants examined in our study produced diminished levels of Ty1 cDNA compared to the BY4743 wild-type strain. One possible model to explain these results would be that these chromatin factors normally play an important role in protecting the Ty1 cDNA from degradation by nucleases. In the absence of these chromatin factors, the Ty1 cDNA is more vulnerable to nuclease digestion, and thus, Ty1 cDNA levels are decreased in such chromatin mutants. This model predicts the existence of an important chromatinized cDNA intermediate that is necessary for retrotransposition. An alternative model would be that these chromatin factors regulate the expression of other genes that, in turn, affect cDNA replication or turnover. Such genes might include some of the other "early" genes identified in our study (Table 1). Additional studies will be required to differentiate between these (and perhaps other) models.

A number of other mutants in our collection also displayed decreased levels of cDNA and thus appear to affect early steps of the retrotransposition cycle. Within the RNA metabolism group, for example, both the *cbc1* and *cbc2* mutants had reduced levels of Ty1 cDNA. The Cbc1 and Cbc2 proteins form a "cap binding complex" that binds to the cap structure of cellular mRNAs (Fortes *et al.*, *Mol. Cell. Biol.* 19:6543-6553, 1999). Therefore, Cbc1 and Cbc2 are likely to affect retrotransposition by binding to either Ty1 mRNA or to other cellular mRNAs that affect retrotransposition. Other mutants in the RNA metabolism group such as *dbr1* also had decreased levels of Ty1 cDNA, consistent with previous reports (Karst *et al.*, *Biochem. Biophys. Res. Comm.* 268:112-117, 2000). The *lsm1* mutant in this group likewise had decreased levels of cDNA (Table 3). In contrast, the remaining four mutants within the RNA metabolism group had normal levels of cDNA.

We also identified 55 mutants that had normal levels of Ty1 cDNA (within a range of plus or minus two-fold of the wild type control levels) as judged by Southern analysis. These mutants are likely to affect one or more of the "late" steps of retrotransposition that occur after the production of cDNA. One of the first steps that must occur after cDNA replication is the nuclear localization of the newly-replicated Ty1 cDNA and integrase. Although it is presently unclear as to how the 6 kb Ty1 cDNA enters the nucleus, Ty1 integrase has a nuclear localization sequence that is required for retrotransposition (Kenna *et al., Mol. Cell. Biol.* 18:1115-1124, 1998; Moore *et al., Mol. Cell. Biol.* 18:1105-1114, 1998). Therefore, integrase enters the nucleus using the normal nuclear import machinery. Two known nuclear pore mutants, *nup84* and *nup133*, were identified in our screen that might affect this step of the retrotranposition cycle. In support of this model, the *nup84* strain has normal levels of cDNA, indicating that it affects a late step of retrotranspostion. The *nup133* mutant has increased levels of Ty1 cDNA that could, in principle, be caused by the accumulation of cDNA in the cytoplasm in the absence of efficient nuclear transport. Finally, the *sin3* mutant identified in our study may also affect the nuclear localization of Ty1 components, since *sin3* affects the nuclear import step of Tf1 retrotransposition in *Schizosaccharomyces pombe* (Dang *et al., Mol. Cell. Biol.* 19:2351-2365, 1999).

Table 3. Mutants with altered cDNA levels

Strain	cDNA level (%BY4743)	Strain	cDNA level (%BY4743)
Control		**Protein Folding/Modification**	
BY4743	100.0	*doa4*	20.1
		mck1	7.1
Chromatin		*nat3*	2.9
ard1	12.3		
nat1	22.9	**Ribosomes/Translation**	
sap30	28.7	*rpl6a*	12.5
sin1	20.1	*rpl19b*	24.2
sin4	22.2	*rpl20b*	16.2
spt4	16.5	*rps10a*	6.1
spt10	15.9		
spt21	12.0	**RNA metabolism**	
stb5	14.6	*cbc1*	12.1
		cbc2	18.4
DNA repair		*dbr1*	18.1
apn1	16.9	*lsm1*	13.6

Nuclear transport		**Transcription**	
Nup133	373.5	*ctk1*	10.5
		pop2	12.9
Miscellaneous		*rtf1*	9.4
bem1	19.6	*rpa49*	8.1
fyv3	15.5	*ssn2*	21.7
hof1	5.2		
jnm1	25.0	**Transcription elongation**	
kcs1	9.9	*thp2*	16.6
mft1	15.6		
		Unknown	
num1	15.1	*ydr496c*	9.7
pat1	8.8	*yor292c*	12.1
scp160	36.3	*ynl226w*	22.3
sec22	14.7	*ynl228w*	19.6
tps2	18.3	*yol159c*	351.1
vps9	41.1		

After entering the nucleus, the cDNA is integrated into chromosomal DNA, primarily near tRNA genes. Despite the large number of host factors identified in our screen, only two factors were identified that affected tRNA gene targeting. A likely explanation for this seemingly small number of targeting mutants is that we only examined the non-essential yeast genes in our study. Because most of the RNA pol III transcription factors are encoded by essential genes, it is likely that we missed at least some targeting factors by focusing only on non-essential yeast genes. Additional screens, focused on essential genes, can be carried out to identify all of the host factors involved in targeting.

After cDNA integration, some level of DNA repair is likely to be required at the integration site, and perhaps at other sites in the yeast genome, to repair damaged DNA that is created during retrotransposition. Four DNA repair mutants were identified in our study. Three of the DNA repair mutants, *mms22*, *rad52*, and *xrs2*, had normal levels of cDNA, and therefore, affected late steps of the retrotransposition cycle. Such factors could be involved in repairing chromosomal DNA damage at integration sites or elsewhere in the genome. The remaining mutant, *apn1*, had significantly decreased levels of cDNA and thus affected an early step of the retrotransposition cycle. The Apn1 protein is an apurinic/apyrimidinic (AP) endonuclease that cleaves DNA at abasic sites in order to facilitate DNA repair. One possible model for Apn1 function would be that it is involved in cDNA repair prior to

integration. If the cDNA were not repaired properly in an *apn1* mutant, we believe the cDNA would be targeted for degradation.

Finally, most of the groups of genes listed in Table 1 contain both "early" and "late" mutants. Therefore, none of the groups appears to be devoted to a single step of the retrotransposition cycle. Nevertheless, some of the groups have a disproportionate number of mutants devoted to either early or late stages of the retrotranspostion cycle. For example, six of the seven transcription elongation mutants (*elp1*, *elp2*, *elp3*, *elp4*, *elp6*, and *kti12*) were found to affect the late stages of retrotransposition. All six of these "late" transcription elongation mutants could, in principle, affect retrotransposition by affecting the transcription of even a single "late" gene. Thus, our screen may have identified groups of genes that are involved in other processes (such as transcription elongation) that are necessary for retrotransposition. This might help to account for the large number of mutants identified in our study. Additional secondary screens and assays will be necessary to identify these groups and to determine how such factors work together to influence retrotransposition.

Although most of the mutants identified in our study retained the ability to target Ty1 integration to tRNA genes, two of the mutants identified, *rit1* and *ctk1*, had diminished levels of tRNA gene targeting in our PCR assay. The Rit1 protein, which is an ADP-ribosylase, is known to modify the methionine tRNA that serves as a primer for Ty1 strong stop synthesis during cDNA replication (Chapman and Boeke, *Cell* 65:483-492, 1991; Astrom and Bystrom, *Cell* 79:535-546, 1994). Therefore, the *rit1* mutant might have been expected to affect cDNA replication. Although the *rit1* strain appeared to have slightly diminished levels of cDNA, the average for the duplicate cDNA measurements was considered to be within the "normal" range (70.5% of wild type). An alternative model would be that *rit1* affects the efficiency of methionine tRNA cleavage from the end of the newly-replicated cDNA (Lauermann and Boeke, *EMBO J.* 16:6603-6612, 1997). If the cDNA lacked the appropriate end structure as a result of faulty end trimming in a *rit1* mutant, it would not be expected to serve as a substrate for Ty1 integrase, and may not be integrated efficiently into the genome. Similar cDNA end mutants have been shown to form multimers that are integrated into the genome by homologous recombination rather than by the normal integrase-mediated mechanism (Sharon *et al.*, *Mol. Cell. Biol.* 14:6540-6551, 1994). Thus, by interfering with

cDNA end processing, *rit1* might promote a shift towards integration by homologous recombination.

We also observed a decrease in tRNA gene targeting in the *ctk1* mutant. Ctk1p is a protein kinase that is known to regulate RNA polymerase II activity by phosphorylating the largest subunit of RNA polymerase II, Rpo21p (Patturajan *et al.*, *J. Biol. Chem.* 274:27823-27828, 1999). One possible explanation for the diminished targeting in this mutant would be that *ctk1* affects the RNA pol II transcription of a presently unknown host factor that is required for efficient targeting. Such factors might include proteins involved in RNA pol III transcription, for example. An alternative model would be that Ctk1p directly regulates RNA polymerase III activity. Since RNA pol III transcription, or an associated activity, is required for efficient tRNA gene targeting, altered phosphorylation of an RNA pol III subunit might be expected to have an impact on Ty1 integration.

A comparison of studies using Gal-Ty1 vs. chromosomal donor elements: Scholes *et al.* (*Genetics* 159:1449-1465, 2001) recently identified a large collection of Ty1 host mutants that had *increased* levels of Ty1 retrotransposition compared to wild type strains (Scholes *et al.*, *supra*). We found little overlap between those Ty1 host mutants and the host factors identified in our screen. The most likely explanation for this result is that Scholes *et al.* screened for mutants with *increased* levels of retrotransposition using a chromosomal Ty1 donor element, whereas we screened for mutants with *decreased* levels of retrotransposition using a Gal-Ty1 donor plasmid. Decreases might be difficult to detect at the already low levels of retrotransposition attained with the chromosomal assay, whereas further increases may not be easily achieved at the relatively high levels of retrotransposition produced with a Gal-Ty1 donor plasmid assay. There also were several other technical differences between these two studies.

A number of additional host factors have been identified that affect the Ty1 retrotransposition cycle (Winston *et al.*, *Genetics* 107:179-197, 1984; Chapman and Boeke, *Cell* 65:483-492, 1991; Boeke and Sandmeyer, In *The Molecular and Cellular Biology of Yeast Saccharomyces: Genome Dynamics, Protein Synthesis, and Energetics*, Eds. Broach *et al.*, pp. 193-261, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1991; Rinkel and Garfinkel, *Genetics* 142:761-776, 1996; Qian *et al.*, *Mol. Cell. Biol.* 18:4783-4792, 1998; Huang *et al.*, *Genetics* 151:1393-1407, 1999; Curcio and Garfinkel, *Trends in*

Genetics 15:43-45, 1999; Bolton *et al.*, *Mol. Cell. Biol.* 9:879-889, 2002). Upon comparing our genome-wide screen with these previous studies, we found that most of the factors identified in our screen were novel. Because our study was limited to the homozygous diploid deletion collection, we did not detect any host factors that were encoded by essential genes. We also did not generally detect *spt* mutants, because we used a *GAL1* promoter instead of the normal LTR promoter to circumvent most of the *spt* mutants. Nevertheless, we did detect four *spt* mutants, *spt2*, *spt4*, *spt10*, and *spt21*, and all four of these had altered levels of Ty1 cDNA. Because these mutants did not affect the *GAL1* promoter used on our Gal-Ty1 plasmid, these *spt* mutants must affect one of the remaining early steps of the retrotransposition cycle leading up to the assembly of virus-like particles and cDNA replication.

As expected, we identified the *dbr1* gene in our screen and observed a decrease in retrotransposition that was similar to the decrease reported previously (Chapman and Boeke, *Cell* 65:483-492, 1991). We also identified the *pmr1* gene in our screen (Bolton *et al.*, *Mol. Cell Biol.* 9:879-889, 2002). Pmr1 is a calcium-transporting ATPase that has been shown to influence the production of Ty1 cDNA (Bolton *et al.*, *supra*). However, *pmr1* was set aside in our study because it did not grow well on YPG medium containing glycerol as the sole carbon source. We used YPG medium as a secondary screen to avoid mutants that could not support respiration and thus might not utilize galactose efficiently in our retrotransposition assay. A total of 86 strains were set aside for this reason, although only a small fraction also had retrotransposition phenoytypes. In the case of *pmr1*, it appears that this secondary screen was too stringent, and led to the elimination of a true positive (Bolton *et al.*, *supra*). However, in most cases, problematic strains were set aside with this secondary screen, and such strains often grew poorly on at least one additional growth medium.

The steady-state levels of Ty1 cDNA are altered in many of the host factor mutants:

We next determined whether the host factor mutants in our collection produced normal levels of Ty1 cDNA. Because double-stranded Ty1 cDNA is produced approximately midway through the retrotransposition cycle, it is a convenient measure of how far the retrotransposition cycle has progressed in a given mutant. Mutants with diminished levels of cDNA would be considered to affect the "early" steps of retrotransposition leading up to virus-like particle assembly and cDNA replication, whereas

mutants with normal levels of cDNA would be considered to affect the "late" steps of retrotransposition that occur after cDNA production.

Interestingly, nine of the ten chromatin mutants examined were found to have significantly decreased levels of Ty1 cDNA compared to the wild type BY4743 control strain (Figure 4A). Therefore, rather than affecting tRNA gene targeting, as we had originally postulated (Table 2), most of the chromatin mutants affected the production (or turnover) of Ty1 cDNA. Upon analyzing all of the mutants in our collection in duplicate by Southern analysis, we found a total of 44 strains with decreased levels of Ty1 cDNA (<50% of wild-type levels), and two mutants with increased levels of cDNA (>200% of wild-type levels; Figure 4 and Table 3). The remaining 55 mutants had normal levels of cDNA (between 50% and 200% of wild type levels; Figure 4 and data not shown). Thus, almost half of the 101 mutants identified in our study affected the early steps of the Ty1 retrotransposition cycle leading up to the formation of virus-like particles and cDNA replication, whereas the remaining half affected the later steps that occur after cDNA replication.

A Prophetic Example

Both Ard1p and Nat1p were identified as yeast host factors that affect Ty1 in our functional genomics screen (described above). Ard1p and Nat1p have been found to work together as a heterodimer and are known to have protein acetyltransferase activity. One of the known substrate targets of the Ard1p/Nat1p heterodimer is a histone. Ard1p/Nat1p are also known to be required for telomeric silencing and silencing at the HML/HMR loci in yeast, and, in addition to the Ty1 phenotype mentioned above, also have several other known phenotypes. Human homologs of Ard1p and Nat1p have been identified (see the tables and figures herein).

Researchers can use existing chemical or drug libraries to screen for compound that bind to Ard1p and/or Nat1p, which may be produced in an expression system (*e.g.*, *E. coli*) using a plasmid designed for that purpose. Tagged versions of these proteins could also be produced and used in conjunction with affinity chromatography columns that bind specifically to the tag for the purpose of purifying such proteins (GST or nickle columns, for example). Ard1p and/or Nat1p could also be expressed in a variety of other *in vitro* and *in vivo* systems such as: an *in vitro* transcription or translation system; an expression system in a vertebrate, such as the SV40 promoter on an Ebna/Orip vector; an expression system in

insect cells, such as the Bacculovirus system; an expression system in yeast; *etc.* Ard1p/Nat1p also could be purified from cells as a native complex using biochemical techniques such as chromatography.

The purified proteins could be used to screen for compounds that bind to the protein. For example, the purified protein could be attached to a solid matrix in a multiple well format, and compound libraries could be screened for binding (one compound being tested per well). By using such high throughput methods, libraries of compounds could be screened. Alternatively, a protein could be exposed to a mixture of compound and those that were bound could be recovered and identified using methods known in the art, such as mass spectroscopy or NMR.

The proteins expressed as described above could also be used to generate antibodies that specifically recognize host factors. Should those antibodies be administered to human patients, they can be humanized.

The proteins expressed as described above could also be used to screen for comjpound that inhibit Ard1p and/or Nat1p acetyltransferase activity *in vitro* or *in vivo*. Alternatively, yeast strains containing intact Ard1p and Nat1p could be used to screen for compounds that inhibit Ard1p/Nat1p acetyltransferase activity. Such strains could also be used to screen for compounds that interfere with known phenotypes of Ard1p and/or Nat1p. Such screening could be done in conjunction with strains in which these genes have been deleted to confirm that Ard1p and/or Nat1p are the targets of such compounds.

An alternative approach is to introduce human homologs of Ard1p and/or Nat1p into yeast and screen for compounds in yeast that inhibit the human activities, including acetyltransferase activity and/or interference with telomeric silencing or other known phenotypes.

Murine homologs of these genes are also known and similar screens could be carried out with those homologs.

Once a compound has been identified, the compound can be tested for activity against a retrovirus. These tests can include applying the compound to human cells before or after the cells are infected with (or exposed to) a retrovirus. Viral titers could be measured using any method available in both treated and untreated controls.

Upon identifying a compound that inhibits viral infection or replication, analogs of such compounds (*e.g.*, analogs bearing different R groups) could be made and tested for enhanced activity or decreased clinical side effects. Antibodies could be optimized for application to humans.

A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

WHAT IS CLAIMED IS:

1. A method for identifying an antiviral compound, the method comprising:

(a) exposing a first cell that expresses a host factor to a candidate compound;

(b) determining whether the candidate compound inhibits the expression or activity of the host factor in the first cell, wherein a candidate compound that inhibits the expression or activity of the host factor in the first cell is a potential antiviral compound;

(c) exposing a second cell to the potential antiviral compound and a retrovirus; and

(d) determining whether the potential antiviral compound inhibits the ability of the retrovirus to infect or replicate within the second cell, wherein a potential antiviral compound that inhibits the ability of the retrovirus to infect the second cell is an antiviral compound.

2. The method of claim 1, wherein the first cell or the second cell is a cell *in vivo*.

3. The method of claim 1, wherein the first cell or the second cell is a cell in cell culture.

4. The method of any of claims 1-3, wherein the first cell is a yeast cell.

5. The method of any of claims 1-3, wherein the first cell is a bacterial cell.

6. The method of claim 5, wherein the bacterial cell is an *E. coli* cell.

7. The method of any of claims 1-3, wherein the first cell is a mammalian cell.

8. The method of claim 7, wherein the mammalian cell is a human cell.

9. The method of claim 1, wherein the first cell or the second cell is a cell of an established cell line.

10. The method of claim 8, wherein the second cell is a T lymphocyte.

11. The method of any of claims 1-3, wherein the first cell and the second cell are cells of the same type.

12. The method of any of claims 1-3, wherein the host factor is an N-terminal acetyltransferase, a histone deacetylase, a histone acetyltransferase, a chromatin factor, inositol hexakisphosphate kinase 3, a high density lipoprotein binding protein, a proton pump in clatherin-coated vesicles, a Rab5 GDP/GTP exchange factor, cyclophilin D, a serine/threonine kinase, ubiquitin specific protease 8, a heat shock protein, an RNA helicase, a ribosomal protein, a nuclear cap binding protein, an RNA lariat debranching enzyme, an Lsm1 protein, a nuclear cap binding protein subunit 1, a 5-methylaminomethyl-2-thiouridylate-methyltransferase, a Ctk1 kinase, a transcription elongation factor or an apoptosis inhibitor, an RNA polymerase II elongator subunit, or an RNA polymerase II associated protein.

13. The method of any of claims 1-3, wherein the host factor is a yeast host factor listed in Table 2, or a biologically active mutant or fragment thereof, a human host factor having an amino acid sequence represented by one of SEQ ID NOs.:1-501 or a biologically active mutant or fragment thereof.

14. The method of claim 13, wherein the host factor further comprises an affinity tag.

15. The method of any of claims 1-3, wherein the candidate compound is an antisense oligonucleotide or an siRNA.

16. The method of any of claims 1-3, wherein the candidate compound is an antibody.

17. The method of any of claims 1-3, wherein the candidate compound is a small molecule.

18. The method of claims 1-3, wherein the retrovirus is a human immunodeficiency virus (HIV).

19. The method of claim 18, wherein the HIV is HIV-1 or HIV-2.

20. The method of claim 1, wherein the retrovirus is a simian or feline immunodeficiency virus (SIV or FIV, respectively) or a human-simian chimeric virus (SHIV).

21. The method of claim 1, wherein the second cell is exposed to the potential antiviral agent before being exposed to the retrovirus.

22. The method of claim 1, wherein the second cell is exposed to the potential antiviral agent after being exposed to the retrovirus.

23. A method for identifying an antiviral compound, the method comprising:

(a) exposing a host factor to a candidate compound;

(b) determining whether the candidate compound binds to or inhibits the expression or activity of the host factor, wherein a candidate compound that binds to the host factor or inhibits the expression or activity of the host factor is a potential antiviral compound;

(c) exposing a cell to the potential antiviral compound and a retrovirus; and

(d) determining whether the potential antiviral compound inhibits the ability of the retrovirus to infect the cell, wherein a potential antiviral compound that inhibits the ability of the retrovirus to infect the cell is an antiviral compound.

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Figure 1.

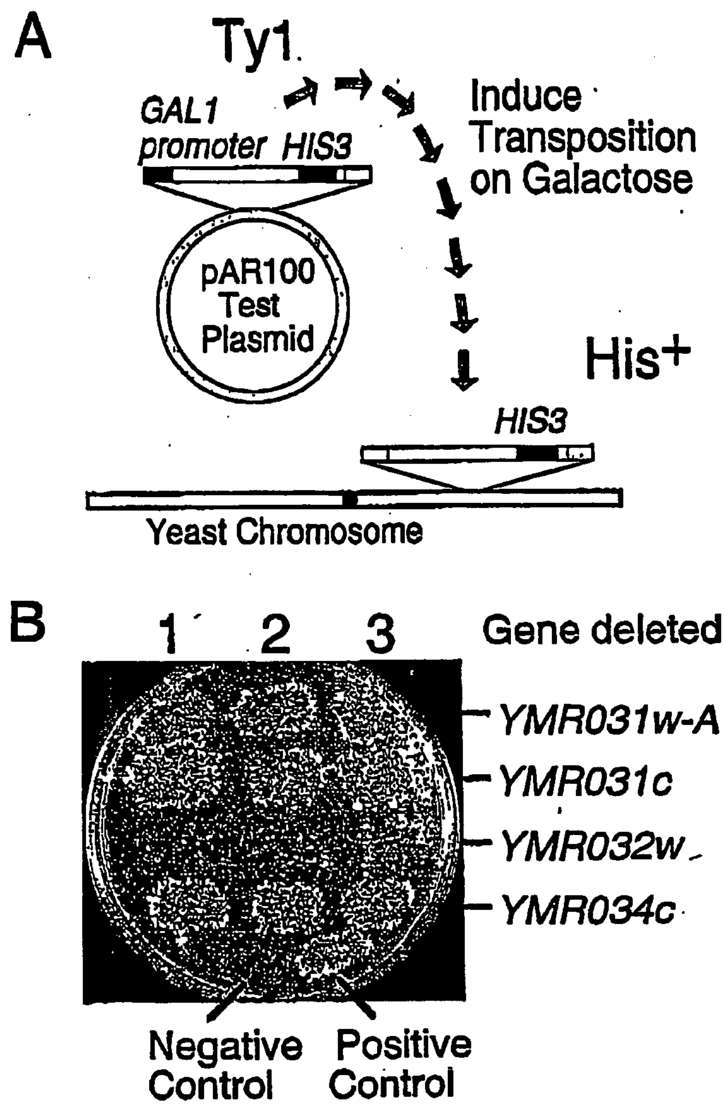
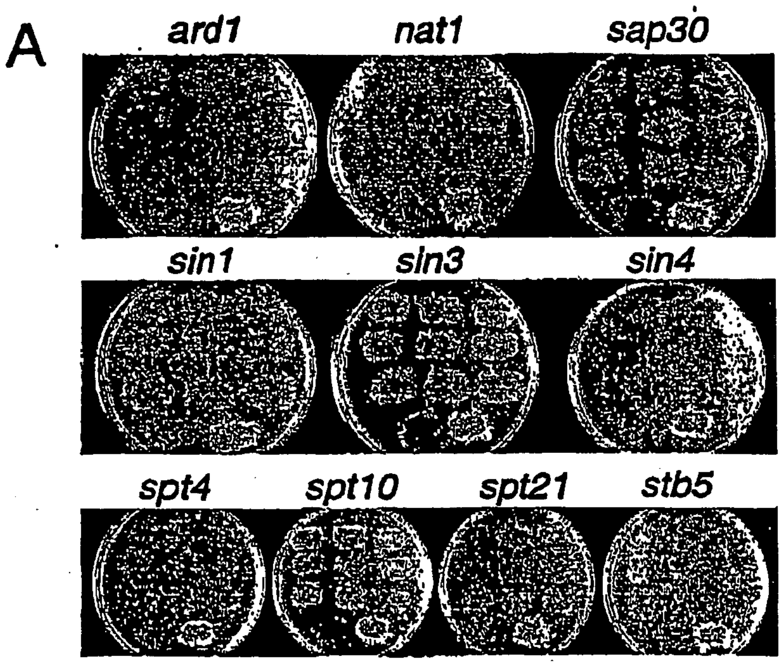
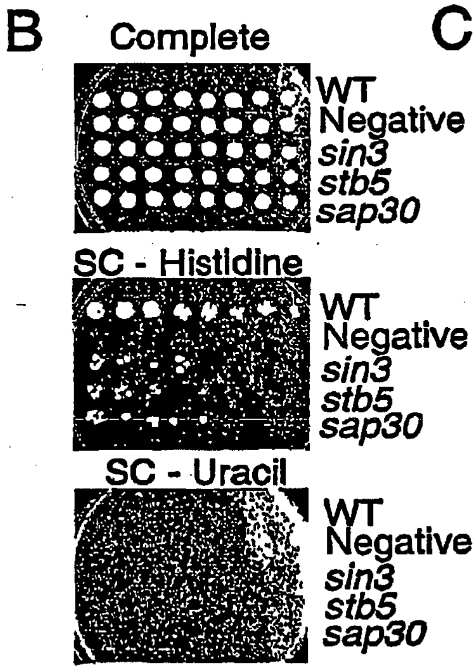

A
Ty1
GAL1
promoter HIS3
pAR100
Test
Plasmid
Induce
Transposition
on Galactose
His+
HIS3
Yeast Chromosome
B
1
2
3
Gene deleted
YMR031w-A
YMR031c
YMR032w
YMR034c
Negative
Control
Positive
Control

Figure 2.

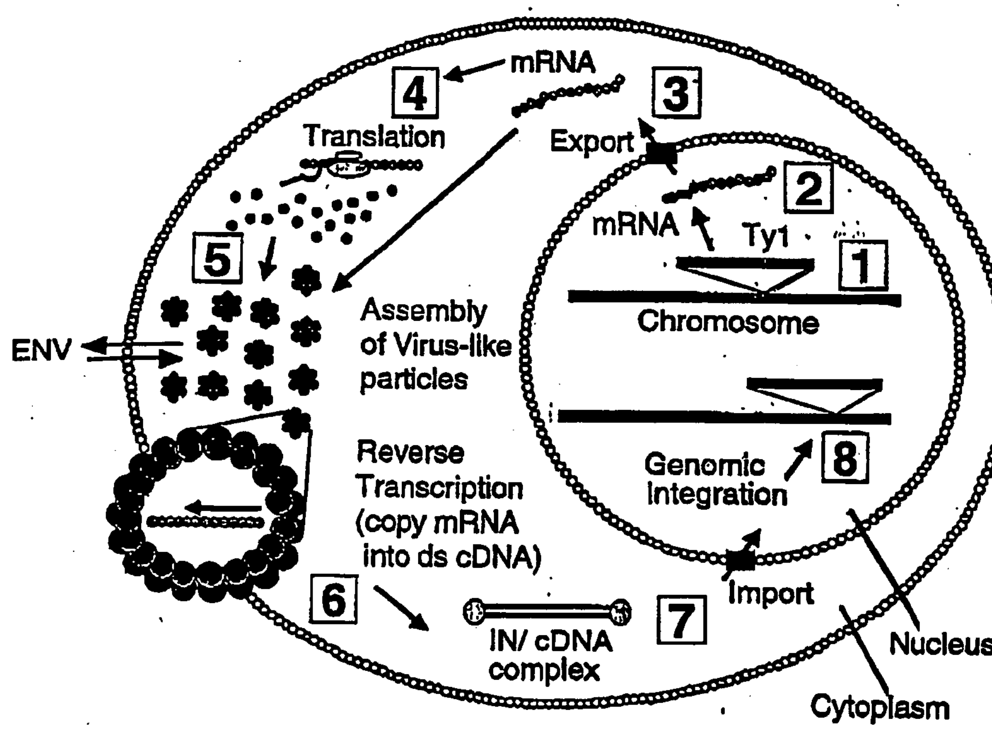




C

Gene	/Fold Δ
ard1	- 32
nat1	- 32
sap30	- 16
sin1	- 16
sin3	- 16
sin4	- 32
spt4	- 32
spt10	- 4
spt21	- 16
stb5	- 32

Figure 3.


mRNA
4
3
Translation
Export
2
mRNA
Ty1
1
5
Chromosome
Assembly
of Virus-like
particles
ENV
Reverse
Transcription
(copy mRNA
into ds cDNA)
Genomic
Integration
8
Import
6
IN/ cDNA
complex
7
Nucleus
Cytoplasm

Human homologs of Ty1 host factors (protein sequences and associated GenBank accession numbers)

Apl5p (11 sequences)

1.
Apl5p human (01) AAC51761
malkmvkgsidrmfdknlqdlvrgirnhkedeakyisqcideikqelkqdniavkanavckltylqmlgydiswaafnii
evmsaskftfkrigylaasqsfhegtdvimlttnqirkdlsspsqydtgvaltglscfvtpdlardlandimtlmshtkp
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idicsqsnyqyitnfewyisilveltrlegtrhghliaaqmldvairvkairkfavsqmsalldsahllasstqrngice
vlyaaawicgefsehlqephhtleamlrprvttlpghiqavyvqnvvklyasilqqkeqageaegaqavtqlmvdrlpqf
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hfscssylittpcysdafakllesgdlsmssikvdgirmsfqnllakicfhhhfsvvervdscasmysrsiqghhvcllv
kkgensvsvdgkcsdstllsnlleemkatlakc (SEQ ID NO:5)

2. Apl5p human (02) AAH10065
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iiklfgaltplgprlgkkliepltnlihstsamsllyecvntviavlislssgmpnhsasiqlcvqklriliedsdqnlk
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sdqyvkleeerrhrqklekdkr (SEQ ID NO:6)

3. Apl5p human (03) AAC34212
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c (SEQ ID NO:7)

4. Apl5p human (04) AAG35473
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sadlevqerascilqlvkhiqklqakdvpvaedfvhccyel (SEQ ID NO:8)

5. Apl5p human (05) NP_003929
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6. Apl5p human (06) AAC34214
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ekldfrlhfscssylittpcysdafakllesgdlsmssikvdgirmsfqnllakicfhhhfsvvervdscasmysrsiqgh
hvcllvkkgensvsvdgkcsdstllsnlleemkatlakc (SEQ ID NO:10)

7. Apl5p human (07) A1G1_HUMAN
mpapirlrelirtirtartqaeeremiqkecaairssfreedntyrcrnvakllymhmlgypahfgqleclkliasqkft
dkrigylgamllldderqdvhllmtnciknldlnhstqfvqglalctlgcmgssemcrdlageveklllktsnsylrkkaalc
avhvirkvpelmemflpatknllneknhgvlhtsvvlltemcerspdmlahfrklvpqlvrilknlimsgyspehdvsgi
sdpflqvrilrllrilgrnddsseamndilaqvatntetsknvgnailyetvltimdiksesglrvlainilgrfllnn
dkniryvaltsllktvqtdhnavqrhrstivdclkdldvsikrramelsfalvngnnirgmmkellyfldscepefkadc
asgiflaaekyapskrwhidtimrvlttagsyvrddavpnliqlitnsvemhaytvqrlykailgdysqqplvqvaawci
geygdllvsgqceeeepiqvtedevldilesvlisnmstsvtrgyaltaimklstrftctvnrikkvvsiygssidvelq
qraveynalfkkydhmrsallermpvmekvttngpteivqtngetepapletkpppsgpqptsqandllidllggnditpv
iptaptskpssaggelldllgdinltgapaaapapasvpqisqphflldglssqplfndiaagipsitayskngIkieft
fersntnpsvtvitiqasnsteldmtdfvfqaavpktfqlqllspsssivpafntgtitqvikvlnpqkqqlrmriklty
nhkgsamqdlaevnnfppqswq (SEQ ID NO:11)

8. Apl5p human (08) NP_001119
mpapirlrelirtirtartqaeeremiqkecaairssfreedntyrcrnvakllymhmlgypahfgqleclkliasqkft
dkrigylgamllldderqdvhllmtnciknldlnhstqfvqglalctlgcmgssemcrdlageveklllktsnsylrkkaalc
avhvirkvpelmemflpatknllneknhgvlhtsvvlltemcerspdmlahfrkslqlvpqlvrilknlimsgyspehdv
sgisdpflqvrilrllrilgrnddsseamndilaqvatntetsknvgnailyetvltimdiksesglrvlainilgrfl
lnndkniryvaltsllktvqtdhnavqrhrstivdclkdldvsikrramelsfalvngnnirgmmkellyfldscepefk
adcasgiflaaekyapskrwhidtimrvlttagsyvrddavpnliqlitnsvemhaytvqrlykailgdysqqplvqvaa
wcigeygdllvsgqceeeepiqvtedevldilesvlisnmstsvtrgyaltaimklstrftctvnrikkvvsiygssidv
elqqraveynalfkkydhmrsallermpvmekvttngpteivqtngetepapletkpppsgpqptsqandllidllggndi
tpviptaptskpssaggelldllgdinltgapaaapapasvpqisqppflldglssqplfndiaagipsitayskngIki
eftfersntnpsvtvitiqasnsteldmtdfvfqaavpktfqlqllspsssivpafntgtitqvikvlnpqkqqlrmrik
ltynhkgsamqdlaevnnfppqswq (SEQ ID NO:12)

9. Apl5p human (09) XP_058218
mpapirlrelirtirtartqaeeremiqkecaairssfreedntyrcrnvakllymhmlgypahfgqleclkliasqkft
dkrigylgamllldderqdvhllmtnciknldlnhstqfvqglalctlgcmgssemcrdlageveklllktsnsylrkkaalc
avhvirkvpelmemflpatknllneknhgvlhtsvvlltemcerspdmlahfrkxxxlvpqlvrilknlimsgyspehdv
sgisdpflqvrilrllrilgrnddsseamndilaqvatntetsknvgnailyetvltimdiksesglrvlainilgrfl
lnndkniryvaltsllktvqtdhnavqrhrstivdclkdldvsikrramelsfalvngnnirgmmkellyfldscepefk
adcasgiflaaekyapskrwhidtimrvlttagsyvrddavpnliqlitnsvemhaytvqrlykailgdysqqplvqvaa
wcigeygdllvsgqceeeepiqvtedevldilesvlisnmstsvtrgyaltaimklstrftctvnrikkvvsiygssidv

elqqraveynalfkkydhmrsallermpvmekvttngpteivqtngetepapletkpppsgpqptsqandlldllggndi
tpviptaptskpssaggelldllgdinltgapaaapapasvpqisqppflldglssqplfndiaagipsitaysknglki
eftfersntnpsvtvitiqasnsteldmtdfvfqaavpktfqlqllspsssivpafntgtitqvikvlnpqkqqlrmrik
ltynhkgsamqdlaevnnfppqswq (SEQ ID NO:13)

10. Apl5p human (10) CAA72902
mpapirlrelirtirtartqaeeremiqkecaairssfreedntyrcrnvakllymhmlgypahfgqleclkliasqkft
dkrigylgamlllderqdvhllmtnciknd lnhstqfvqglalctlgcmgssemcrdlagevekllktsnsylrkkaalc
avhvirkvpelmemflpatknllneknhgvlhtsvvlltemcerspdmlahfrkneklvpqlvrilknlimsgyspehdv
sgisdpflqvrilrllrilgrndddsseamndilaqvatntetsknvgnailyetvltimdiksesglrvlainilgrfl
lnndkniryvaltsllktvqtdhnavqrhrstivdclkdldvsikrramelsfalvngnnirgmmkellyfldscepefk
adcasgiflaaekyapskrwhidtimrvlttagsyvrddavpnliqlitnsvemhaytvqrlykailgdysqqplvqvaa
wcigeygdllvsgqceeeepiqvtedevldilesvlisnmstsvtrgyaltaimklstrftctvnrikkvvsiygssidv
elqqraveynalfkkydhmrsallermpvmekvttngpteivqtngetepapletkpppsgpqptsqandlldllggndi
tpviptaptskpssaggelldllgdinltgapaaapapasvpqisqppflldglssqplfndiaagipsitaysknglki
eftfersntnpsvtvitiqasnsteldmtdfvfqaavpktfqlqllspsssivpafntgtitqvikvlnpqkqqlrmrik
ltynhkgsamqdlaevnnfppqswq (SEQ ID NO:14)

11. Apl5p human (11) AAC67390
mvvpslklqdlieeirgaktqaqereviqkecahirasfrdgdpvhrhrqlakllyvhmlgypahfgqmeclkliassrf
tdkrvgylgamlllderhdahllitnsikndlsqgiqpvqglalctlstmgsaemcrdlapeveklllqpspyvrkkail
~~tavhmirkvpelssvflppcaqllherhhgillgtitlitelcgrnpaalrhfrkvvpqlvhilrtlvtmgystehsisg~~
vsdpflqvqilrllrilgrnheessetmndllaqvatntdtsrnagnavlfetvltimdirsaaglrvlavnilgrflln
sdrniryvaltsllrlvqsdhsavqrhrptvveclretdaslsrralelslalvnssnvrammqelqaflescppdlrcd
cdsgillaaerfapttrwhidtilhvltsagthvrddaaghtltqliggaqelhaysvrrlynalaedisqqplvqvaaw
cigeygdlllagnceeieplqvdeeevlallekvlqshmslpatrgyaltalmklstrlcgdnnrirqvvsiygscldve
lqqraveydtlfrkydhmraailekmplverdgpqadeeakeskeaaqlseaapvptepqasqlldlldlldgasgdvqh
pphldpspggalvhlldlpcvppppapipdlkvferegvqlnlsfirppenpalllititatnfsegdvthfilpgccaq
espaaaagpqwehssssgwpsyhpalqnpqs (SEQ ID NO:15)

__Ard1p (1 sequence)__

12. Ard1p human NP_003482
mnirnarpedlmnmqhcnllclpenyqmkyyfyhglswpqlsyiaedengkivgyvlakmeedpddvphghitslav
krshrrlglaqklmdqasramienfnakyvslhvrksnraalhlysntlnfqisevepkyyadgedayamkrdltqmadel
rrhlelkekgrhvvlgaienkveskgnsppssgeacreekglaaedsggdskdlsevsettestdvkdsseasdsas (SEQ ID NO:16)

__Cbc2p (11 sequences)__

13. Cbc2p human (01) XP_028279
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:17)

14. Cbc2p human (02) NP_031388
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:18)

15. Cbc2p human (03) P52298
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:19)

16. Cbc2p human (04) I37222
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:20)

17. Cbc2p human (05) CAA58962
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:21)

18. Cbc2p human (06) AAH01255
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:22)

19. Cbc2p human (07) 1582342
msggllkalrsdsyvelsqyrdqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmkkta
cgfcfveyysradaenamryingtrlddriirtdwdagfkegrqygrgrsggqvrdeyrqdydagrggygklaqnq
(SEQ ID NO:23)

20. Cbc2p human (08) CAD19101
lscyrdhqfsgrkfqqekllkesstlnmgnlsfytteekihelfsrsdirnifmgldkikktacgfcfvechnradaena
mrfltgtcldewiictdwdvgfregqqygrgksggq (SEQ ID NO:24)

Figure 4

21. Cbc2p human (09) 15988386
dqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmktacgfcfveyysradaenamryin gtrlddriirtdwdagfk (SEQ ID NO:25)

22. Cbc2p human (10) 20151224
dqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmktacgfcfveyysradaenamryin gtrlddriirtdwdagfk (SEQ ID NO:26)

23. Cbc2p human (11) 20151225
dqhfrgdneeqekllkksctlyvgnlsfytteeqiyelfsksgdikkiimgldkmktacgfcfveyysradaenamryin gtrlddriirtdwdagfk (SEQ ID NO:27)

<u>**Cpr7p (5 sequences)**</u>

24. Cpr7p human (01) NP_005029
mshpspqakpsnpsnprvffdvdiggervgrivlelfadivpktaenfralctgekgighttgkplhfkgcpfhriikkf miqggdfsnqngtggesiygekfedenfhykhdregllsmanagrntngsqffittvptphldgkhvvfgqvikgigvar ilenvevkgekpaklcviaecgelkegddggifpkdgsgdshpdfpedadidlkdvdkillitedlknigntffksqnwe maikkyaevlryvdsskavietadraklqpialscvlnigacklkmsnwqgaidscleaeldpsntkalyrraqgwqgl keydqaladlkkaqgiapedkaiqaellkvkqkikaqkdkekavyakmfa (SEQ ID NO:28)

25. Cpr7p human (02) AAH01555
mgikvqrprcffdiainnqpagrvvfelfsdvcpktcenfrclctgekgtgkstqkplhykscllfhrvvkdfmvqggdfs egngrggesiyggffedesfavkhnkefllsmanrgkdtngsqffittkptphldghhvvfgqvisgqevvreienqktd aaskpfaevrilscgelipkskvkkeekkrhksssssssssdsdsssdsqsssdssdsesateekskkrkkkhrknsrk hkkekkkrkkskksasseseaenleaqpqstvrpeeippipenrflmrksppkadekerknrerererecnppnsqpasy qrrllvtrsgrkikgrgprvgdsfprdlhniafvflk (SEQ ID NO:29)

26. Cpr7p human (03) A47328
mgensvalggpawgrrrrsvsgvgvwlqwqcflfcsrgpaqaggqpalaatsvamgaqdrpqchfdieinrepvgrimf qlfsdicpktcknflclcsgekglgkttgkklcykgstfhrvvknfmiqggdfsegngkggesiyggyfkdenfilkhdra fllsmanrgkhtngsqffittkpaphldgvhvvfglvisgfevieqienlktdaasrpyadvrvidcgvlatksikdvfe kkrkkpthsegsdsssnsssssesssesel ehersrrrkhkrrpkvkrskkrrkeassseeprnkhamnpkghsersdtn ekrsvdssakrekpvvrpeeippvpenrfllrrdmpvvtaepepkipdvapivsdqkpsvsksgrkikgrgtiryhtppr srscsesddddssetpphwkeemqrlrayrppsgekwskgdklsdpcssrwderslsqrsrswsyngyysdlstarhsgh hkkrrkekkvkhkkkgkkqkhcrrhkqtkkrrilipsdiesskssttrrmksscdrerssrssslsshhsskrdwsksdkd vqsslthssrdsyrskshsqsysrgssrsrtaskssshsrsrsksrsssksghrkrasksprktasqlsenkpvkteplr atmaqnenvvvqpvvaenipviplsdspppsrwkpgekpwkpsyeriqemkakttthllpiqstyslaniketgssssyhk

reknsesdqstyskysdrssessprsrsrssrsrsysrsytrsrslasshsrsrspssrshsrnkysdhsqcsrsssyts issddgrrakrrlrssgkknsvshkkhssssektlhskyvkgrdrsscvrkysesrssldyssdseqssvqatqsaqeke kqgqmerthnkqeknrgeekskserecphskkrtlkenlsdhlrngskpkrknyagskwdsesnserdvtknskndshp ssdkeegeatsdsesevseihikvkpttkssintslpddngawksskqrtstsdsegscsnsennrgkpqkhkhgskenlk rehtkkvkeklkgkkdkkhkapkrkqafhwqpplefgeeeeeeiddkqvtqeskekkvsennetikdnilkteksseedl sgkhdtvtvssdldqftkddsklsisptalnteenvaclqniqhveesvpngvedvlqtddnmeictpdrsspakveets plgnarldtpdinivlkqdmatehpqaevvkqessmseskvlgevgkqdsssaslasagestgkkevaeksqinlidkkw kplqgvgnlaapnaatssavevkvlttvpemkpqglrieiksknkvrpgslfdevrktarlnrrprnqesssdeqtpsrd ddsqsrspsrsrsksetksrhrtrsvsyshsrsrsrsstssyr (SEQ ID NO:30)

27. Cpr7p human (04) NP_005376
mgaqdrpqchfdieinrepvgrimfqlfsdicpktcknflclcsgekglgkttgkklcykgstfhrvvknfmiqggdfse gngkggesiyggyfkdenfilkhdrafllsmanrgkhtngsqffittkpaphldgvhvvfglvisgfevieqienlktda asrpyadvrvidcgvlatksikdvfekkrkkpthsegsdsssnsssssesssesele hersrrrkhkrrpkvkrskkrrk eassseeprnkhamnpkghsersdtnekrsvdssakrekpvvrpeeippvpenrfllrrdmpvvtaepepkipdvapivs dqkpsvsksgrkikgrgtiryhtpprsrscsesddddssetpphwkeemqrlrayrppsgekwskgdklsdpcssrwder slsqrsrswsyngyysdlstarhsghhkkrrkekkvkhkkkgkkqkhcrrhkqtkkrrilipsdiessksstrrmksscd rerssrsssIsshhsskrdwsksdkdvqsslthssrdsyrskshsqsysrgssrsrtaskssshsrsrsksrsssksghr kraskspr ktasqlsenkpvkteplratmaqnenvvvqpvvaenipviplsdspppsrwkpgqkpwkpsyeriqemka ktthllpiqstyslaniketgssssyhkreknsesdqstyskysdrssessprsrsrssrsrsysrsytrsrslasshsrsr spssrshsrnkysdhsqcsrsssytsissddgrrakrrlrssgkknsvshkkhssssektlhskyvkgrdrsscvrkyse srssldyssdseqssvqatqsaqekekqgqmerthnkqeknrgeekskserecphskkrtlkenlsdhlrngskpkrkny agskwdsesnserdvtknskndshpssdkeegeatsdsesevseihikvkpttkssintslpddngawksskqrtstsds egscsnsennrgkpqkhkhgskenlkrehtkkvkeklkgkkdkkhkapkrkqafhwqpplefgeeeeeeiddkqvtqe skekkvsennetikdnilkteksseedlsgkhdtvtvssdldqftkddsklsisptalnteenvaclqniqhveesvpngve dvlqtddnmeictpdrsspakveetsplgnarldtpdinivlkqdmatehpqaevvkqessmseskvlgevgkqdsssas lasagestgkkevaeksqinlidkkwkplqgvgnlaapnaatssavevkvlttvpemkpqglrieiksknkvrpgslfde vrktarlnrrprnqesssdeqtpsrdddsqsrspsrsrsksetksrhrtrsvsyshsrsrsrsstssyrsrsysrsrsrg wysrgrtrsrsssyrsykshrtssrsrsrsssydphsrsrsytydsyysrsrsrsrsqrsdsyhrgrsynrrsrscrsyg sdsesdrsyshhrspsessrys (SEQ ID NO:31)

28. Cpr7p human (05) NP_004783
mgikvqrprcffdiainnqpagrvvfelfsdvcpktcenfrclctgekgtgkstqkplhykscIfhrvvkdfmvqggdfs egngrggesiyggffedesfavkhnkefllsmanrgkdtngsqffittkptphldghhvvfgqvisgqevvreienqktd aaskpfaevrilscgelipkskvkkeekkrhksssssssssdsdsssdsqsssdssdsesateekskkrkkkhrknsrk hkkekkkrkkskksasseseaenleaqpqstvrpeeippipenrflmrksppkadekerknrerererecnppnsqpasy qrrllvtrsgrkikgrgprryrtpsrsrsrdrfrrsetpphwrqemqraqrmrvssgerwikgdkselneikenqrspvr vkerkitdhrnvsespnrknekekkvkdhksnskerdirrnsekddkyknkvkkrakskrskskekskskerdskhnrn eekrmrsrskgrdhenvkekekqsdskgkdqersrskekskqlesksnehdhskskekdrraqsrsrecditkgkhsyns rtrersrsrdrsrrvrsrthdrdrsrskeyhryreqeyrrrgrsrsrerrtppgrsrskdrrrrrrdsrssereesqsrn kdkyrnqesksshrkensesekrmysksrdhnssnnsrekkadrdqspfskikqssqddelkssmlknkedekirssvek enqkskgqendhvheknkkfdhesspgtdedksg (SEQ ID NO:32)

Ctk1p (41 sequences)

29. Ctk1p human (01) BAA74927
sssrsrhssispvrlplnsslgaelsrkkkeraaaaaaakmdgkessyersgsysgrspspygrrrssspflskrslsrs
plpsrksmksrsrspaysrhssshskkkrsssrsrhssispvrlplnsslgaelsrkkkeraaaaaaakmdgkeskgspv
flprkenssveakdsgleskklprsvkleksapdtelvnvthlntevknssdtgkvkldensekhlvkdlkaqgtrdskp
ialkeeivtpketetseketppplptiasppplplptttpppqtpplpplppipalpqqpplppsqpafsqvpasststlp
psthsktsavssqansqppvqvsvktqvsvtaaiphlktstlpplplppllpgdddmdspketlpskpvkkekeqrtrhl
ltdlplppelpggdlsppdspepkaitppqqpykkrpkiccprygerrqtesdwgkrcvdkfdiigiigegtygqvykak
dkdtgelvalkkvrldnekegfpitaireikilrqlihrsvvnmkeivtdkqdaldfkkdkgafylvfeymdhdlmglle
sglvhfsedhiksfmkqlmegleychkknflhrdikcsnillnnsgqikladfglarlynseesrpytnkvitlwyrppe
lllgeerytpaidvwscgcilgelftkkpifqanlelaqlelisrlcgspcpavwpdviklpyfntmkpkkqyrrrlree
fsfipsaaldlldhmltldpskrctaeqtlqsdflkdvelskmappdlphwqdchelwskkrrrqrqsgvvveepppskt
srkettsgtstepvknsspappqpapgkvesgagdaigladitqqlnqselavllnllqsqtdlsipqmaqllnihsnpe
mqqqlealnqsisalteatsqqqdsetmapeeslkeapsapvilpsaeqttleasstpadmqnilavllsqlmktqepag
sleennsdknsgpqgprrtptmpqeeaagrsnggnal (SEQ ID NO:33)

30. Ctk1p human (02) NP_057591
mpnserhggkkdgsggasgtlqpssgggssnsrerhrlvskhkrhkskhskdmglvtpeaaslgtvikplveyddissds
dtfsddmafkldrrenderrgsdrsdrlhkhrhhqhrrsrdllkakqtekeksqevssksgsmkdrisgsskrsneetdd
ygkaqvaksssskesrssklhkekterkerelksghkdrskshrkretpksyktvdspkrrsrsphrkwsdsskqddspsga
sygqdydlspsrshtssnydsykkspgstsrrqsvsppykepsayqsstrspspysrrqrsvspysrrrsssyersgsys
grspspygrrrssspflskrslsrsplpsrksmksrsrspaysrhssshskkkrsssrsrhssispvrlplnsslgaels
rkkkeraaaaaaakmdgkeskgspvflprkenssveakdsgleskklprsvkleksapdtelvnvthlntevknssdtgk
vkldensekhlvkdlkaqgtrdskpialkeeivtpketetseketppplptiasppplplptttpppqtpplpplppipal
pqqpplppsqpafsqvpasststlppsthsktsavssqansqppvqvsvktqvsvtaaiphlktstlpplplppllpggd
dmdspketlpskpvkkekeqrtrhlltdlplppelpggdlsppdspepkaitppqqpykkrpkiccprygerrqtesdwg
krcvdkfdiigiigegtygqvykardkdtgelvalkkvrldnekegfpitaireikilrqlihrsvvnmkeivtdkqdal
dfkkdkgafylvfeymdhdlmgllesglvhfsedhiksfmkqlmegleychkknflhrdikcsnillnnsgqikladfgl
arlynseesrpytnkvitlwyrppelllgeerytpaidvwscgcilgelftkkpifqanlelaqlelisrlcgspcpavw
pdviklpyfntmkpkkqyrrrlreefsfipsaaldlldhmltldpskrctaeqtlqsdflkdvelskmappdlphwqdch
elwskkrrrqrqsgvvveepppsktsrkettsgtstepvknsspappqpapgkvesgagdaigladitqqlnqselavll
nllqsqtdlsipqmaqllnihsnpemqqqlealnqsisalteatsqqqdsetmapeeslkeapsapvilpsaeqmtleas
stpadmqnilavllsqlmktqepagsleennsdknsgpqgprrtptmpqeeaaacpphilppekrppeppgppppppp
plvegdlssapqelnpavtaallqllsqpeaeppghlphehqalrpmeystrprpnrtygntdgpetgfsaidtdernsgp
alteslvqtlvknrtfsgslshlgesssyqgtgsvqfpgdqdlrfarvplalhpvvgqpflkaegssnsvvhaetklqny
gelgpgttgasssgaglhwggptqssaygklyrgptrvpprggrgrgvpy (SEQ ID NO:34)

31. Ctk1p human (03) Q9NYV4
mpnserhggkkdgsggasgtlqpssgggssnsrerhrlvskhkrhkskhskdmglvtpeaaslgtvikplveyddissds
dtfsddmafkldrrenderrgsdrsdrlhkhrhhqhrrsrdllkakqtekeksqevssksgsmkdrisgsskrsneetdd
ygkaqvaksssskesrssklhkektrkerelksghkdrskshrkretpksyktvdspkrrsrsphrkwsdsskqddspsga
sygqdydlspsrshtssnydsykkspgstsrrqsvsppykepsayqsstrspspysrrqrsvspysrrrsssyersgsys

grspspygrrrsssspflskrslsrsplpsrksmksrsrspaysrhssshskkkrsssrsrhssispvrlplnsslgaels
rkkkeraaaaaaakmdgkeskgspvflprkenssveakdsgleskklprsvkleksapdtelvnvthlntevknssdtgk
vkldensekhlvkdlkaqgtrdskpialkeeivtpketetseketppplptiasppppplptttpppqtpplpplppipal
pqqpplppsqpafsqvpasststlppsthsktsavssqansqppvqvsvktqvsvtaaiphlktstlpplplppllpggd
dmdspketlpskpvkkekeqrtrhlltdlplppelpggdlsppdspepkaitppqqpykkrpkiccprygerrqtesdwg
krcvdkfdiigiigegtygqvykardkdtgelvalkkvrldnekegfpitaireikilrqlihrsvvnmkeivtdkqdal
dfkkdkgafylvfeymdhdlmgllesglvhfsedhiksfmkqlmegleychkknflhrdikcsnillnnsgqikladfgl
arlynseesrpytnkvitlwyrppelllgeerytpaidvwscgcilgelftkkpifqanlelaqlelisrlcgspcpavw
pdviklpyfntmkpkkqyrrrlreefsfipsaaldlldhmltldpskrctaeqtlqsdflkdvelskmappdlphwqdch
elwskkrrrqrqsgvvveepppsktsrkettsgtstepvknsspappqpapgkvesgagdaigladitqqlnqselavll
nllqsqtdlsipqmaqllnihsnpemqqqlealnqsisalteatsqqqdsetmapeeslkeapsapvilpsaeqmtleas
stpadmqnilavllsqlmktqepagsleennsdknsgpqgprrtptmpqeeaaacpphilppekrppeppgppppppp
plvegdlssapqelnpavtaallqllsqpeaeppghlphehqalrpmeystrprpnrtygntdgpetgfsaidtdernsgp
alteslvqtlvknrtfsgslshlgesssyqgtgsvqfpgdqdlrfarvplalhpvvgqpflkaegssnsvvhaetklqny
gelgpgttgasssgaglhwggptqssaygklyrgptrvpprggrgrgvpy (SEQ ID NO:35)

32. Ctk1p human (04) AAF36401
mpnserhggkkdgsggasgtlqpssgggssnsrerhrlvskhkrhkskhskdmglvtpeaaslgtvikplveyddissds
dtfsddmafkldrrenderrgsdrsdrlhkhrhhqhrrsrdllkakqtekeksqevssksgsmkdrisgsskrsneetdd
ygkaqvakssskesrssklhkektrkerelksghkdrskshrkretpksyktvdspkrrsrsphrkwsdsskqddspsga
sygqdydlspsrshtssnydsykkspgstsrrqsvsppykepsayqsstrspspysrrqrsvspysrrrsssyersgsys
grspspygrrrsssspflskrslsrsplpsrksmksrsrspaysrhssshskkkrsssrsrhssispvrlplnsslgaels
rkkkeraaaaaaakmdgkeskgspvflprkenssveakdsgleskklprsvkleksapdtelvnvthlntevknssdtgk
vkldensekhlvkdlkaqgtrdskpialkeeivtpketetseketppplptiasppppplptttpppqtpplpplppipal
pqqpplppsqpafsqvpasststlppsthsktsavssqansqppvqvsvktqvsvtaaiphlktstlpplplppllpggd
dmdspketlpskpvkkekeqrtrhlltdlplppelpggdlsppdspepkaitppqqpykkrpkiccprygerrqtesdwg
krcvdkfdiigiigegtygqvykardkdtgelvalkkvrldnekegfpitaireikilrqlihrsvvnmkeivtdkqdal
dfkkdkgafylvfeymdhdlmgllesglvhfsedhiksfmkqlmegleychkknflhrdikcsnillnnsgqikladfgl
arlynseesrpytnkvitlwyrppelllgeerytpaidvwscgcilgelftkkpifqanlelaqlelisrlcgspcpavw
pdviklpyfntmkpkkqyrrrlreefsfipsaaldlldhmltldpskrctaeqtlqsdflkdvelskmappdlphwqdch
elwskkrrrqrqsgvvveepppsktsrkettsgtstepvknsspappqpapgkvesgagdaigladitqqlnqselavll
nllqsqtdlsipqmaqllnihsnpemqqqlealnqsisalteatsqqqdsetmapeeslkeapsapvilpsaeqmtleas
stpadmqnilavllsqlmktqepagsleennsdknsgpqgprrtptmpqeeaaacpphilppekrppeppgppppppp
plvegdlssapqelnpavtaallqllsqpeaeppghlphehqalrpmeystrprpnrtygntdgpetgfsaidtdernsgp
alteslvqtlvknrtfsgslshlgesssyqgtgsvqfpgdqdlrfarvplalhpvvgqpflkaegssnsvvhaetklqny
gelgpgttgasssgaglhwggptqssaygklyrgptrvpprggrgrgvpy (SEQ ID NO:36)

33. Ctk1p human (05) Q14004
mlpedkeadslrgnisvkavkkevekklrclladlplppelpggddlskspeekkttqlhskrrpkicgprygetkekd
idwgklcvdkfdiigiigegtygqvykardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdk
edaldfkkdkgafylvfeymdhdlmgllesglvhfyenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikla
dfglarlysseesrpytnkvitlwyrppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspc
pavwpdviklpyfntmkpkkqyrrklreefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskclhqislyg
kivmsygvkseedrsrwa (SEQ ID NO:37)

Figure 4

34. Ctk1p human (06) AAA58424
mlpedkeadslrgnisvkavkkevekklrclladlplppelpggddlskspeekktttqlhskrrpkicgprygetkekd
idwgklcvdkfdiigiigegtygqvykardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdk
edaldfkkdkgafylvfeymdhdlmgllesglvhfyenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikla
dfglarlysseesrpytnkvitlwyrppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspc
pavwpdviklpyfntmkpkkqyrrklreefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskclhqislyg
kivmsygvkseedrsrwa (SEQ ID NO:38)

35. Ctk1p human (07) A38197
mlpedkeadslrgnisvkavkkevekklrclladlplppelpggddlskspeekktttqlhskrrpkicgprygetkekd
idwgklcvdkfdiigiigegtygqvykardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdk
edaldfkkdkgafyvafeymdhdlmgllesglvhfyenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikla
dfglarlysseesrpytnkvitlwyrppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspc
pavwpdviklpyfntmkpkkqyrrklreefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskclhqislyg
kivmsygvkseedrsrwa (SEQ ID NO:39)

36. Ctk1p human (08) NP_112557
mpsssdtalggggglswaekrleerrkrrrflspqqppllplllqpqllqppppppllflaapgtaaaaaaaaasssc
fspgpplevkrlargkrraggrqkrrrgpragqeaekrrvfslpqpqqdggggassgggvtplveyedvssqseqglllg
gasaataataaggtggsggspasssgtqrrgegserrprrdrrsssgrskerhrehrrrdgqrggseasksrsrhshsge
eraevaksgssssggrrksasatssssssrkdrdskahrsrtksskeppsaykeppkayredktepkayrrrrslsplg
grddspvshrasqslrsrkspspagggsspysrrlprspspysrrrspsysrhssyerggdvspspysssswrrsrspys
pvlrrsgksrsrspyssrhsrsrsrhrlsrsrsrhssispstltlkssiaaelnknkkaraaeaaraaeaakaaeatkaa
eaaakaakasntstptkgntetsasasqtnhvkdvkkikiehapspssggtlkndkaktkpplqvtkvennlivdkatkk
avivgkesksaatkeesvslkektkpltpsigakekeqhvalvtstlpplplppmlpedkeadslrgnisvkavkkevek
klrclladlplppelpggddlskspeekktttqlhskrrpkicgprygetkekdidwgklcvdkfdiigiigegtygqvy
kardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdkedaldfkkdkgafylvfeymdhdlmg
llesglvhfnenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikladfglarlysseesrpytnkvitlwyr
ppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspcpavwpdviklpyfntmkpkkqyrrkl
reefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskmpppdlplwqdchelwskkrrrqkqmgmtddvsti
kaprkdlslglddsrtntpqgvlpssqlksqgssnvapgekqtdpstpqqesskplggiqpssqtiqpkmetdaaqaavq
safavlltqlikaqqskqkdvlleerengsgheaslqlrpppepstpvsgqddliqhqdmrileltpepdrprilppdqr
ppeppepppvteedldyrtenqhvpttsssltdphagvkaallqllaqhqpqddpkreggidyqagdtyvstsdykdnfg
sssfssapyvsndglgsssapplerrsfignsdiqsldnystasshsggppqpsafsesfpssvagygdiylnagpmlfs
gdkdhrfeyshgpiavlanssdpstgpesthplpakmhnynyggnlqenpsgpslmhgqtwtspaqgpgysqgyrghi
ststgrgrgrglpy (SEQ ID NO:40)

37. Ctk1p human (09) CAC10401
mpsssdtalggggglswaekrleerrkrrrflspqqppllplllqpqllqppppppllflaapgtaaaaaaaaasssc
fspgpplevkrlargkrraggrqkrrrgpragqeaekrrvfslpqpqqdggggassgggvtplveyedvssqseqglllg
gasaataataaggtggsggspasssgtqrrgegserrprrdrrsssgrskerhrehrrrdgqrggseasksrsrhshsge

eraevaksgsssssggrrksasatssssssrkdrdskahrsrtksskeppsaykeppkayredktepkayrrrrslsplg grddspvshrasqslrsrkspspagggsspysrrlprspspysrrrspsysrhssyerggdvspspyssssswrrsrspys pvlrrsgksrsrspyssrhsrsrsrhrlsrsrsrhssispstltlkssIaaelnknkkaraaeaaraaeaakaaeatkaa eaaakaakasntstptkgntetsasasqtnhvkdvkkikiehapspssggtlkndkaktkpplqvtkvennlivdkatkk avivgkesksaatkeesvslkektkpltpsigakekeqhvalvtstlpplplppmlpedkeadslrgnisvkavkkevek klrclladlplppelpggddlskspeekktttqlhskrrpkicgprygetkekdidwgklcvdkfdiigiigegtygqvy kardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdkedaldfkkdkgafylvfeymdhdlmg llesglvhfnenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikladfglarlysseesrpytnkvitlwyr ppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspcpavwpdviklpyfntmkpkkqyrrkl reefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskmpppdlplwqdchelwskkrrrqkqmgmtddvsti kaprkdlslglddsrtntpqgvlpssqlksqgssnvapgekqtdpstpqqesskplggiqpssqtiqpkmetdaaqaavq safavlltqlikaqqskqkdvlleerengsgheaslqlrpppepstpvsgqddliqhqdmrileltpepdrprilppdqr ppeppepppvteedldyrtenqhvpttsssltdphagvkaallqllaqhqpqddpkreggidyqagdtyvstsdykdnfg sssfssapyvsndglgsssapplerrsfignsdiqsldnystasshsggppqpsafsesfpssvagygdiylnagpmlfs gdkdhrfeyshgpiavlanssdpstgpesthplpakmhnynyggnlqenpsgpslmhgqtwtspaqgpgysqgyrghi ststgrgrgrglpy (SEQ ID NO:41)

38. Ctk1p human (10) NP_003709
mpsssdtalggggglswaekrleerrkrrrflspqqppllIpllqpqllqppppppplIflaapgtaaaaaaaaaasssc fspgpplevkrlargkrraggrqkrrrgpragqeaekrrvfslpqpqqdggggassgggvtplveyedvssqseqglllg gasaataataaggtggsggspasssgtqrrgegserrprrdrrsssgrskerhrehrrrdgqrggseasksrsrhshsge eraevaksgsssssggrrksasatssssssrkdrdskahrsrtksskeppsaykeppkayredktepkayrrrrslsplg grddspvshrasqslrsrkspspagggsspysrrlprspspysrrrspsysrhssyerggdvspspyssssswrrsrspys pvlrrsgksrsrspyssrhsrsrsrhrlsrsrsrhssispstltlkssIaaelnknkkaraaeaaraaeaakaaeatkaa eaaakaakasntstptkgntetsasasqtnhvkdvkkikiehapspssggtlkndkaktkpplqvtkvennlivdkatkk avivgkesksaatkeesvslkektkpltpsigakekeqhvalvtstlpplplppmlpedkeadslrgnisvkavkkevek klrclladlplppelpggddlskspeekktttqlhskrrpkicgprygetkekdidwgklcvdkfdiigiigegtygqvy kardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdkedaldfkkdkgafylvfeymdhdlmg llesglvhfnenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikladfglarlysseesrpytnkvitlwyr ppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspcpavwpdviklpyfntmkpkkqyrrkl reefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskmpppdlplwqdchelwskkrrrqkqmgmtddvsti kaprkdlslglddsrtntpqgvlpssqlksqgssnvapvktgpgqhlnhselaillnllqsktsvnmadfvqvlnikvns etqqqlnkinlpagilatgekqtdpstpqqesskplggiqpssqtiqpkmetdaaqaavqsafavlltqlikaqqskqkd vlleerengsgheaslqlrpppepstpvsgqddliqhqdmrileltpepdrprilppdqrppeppepppvteedldyrte nqhvpttsssltdphagvkaallqllaqhqpqddpkreggidyqagdtyvstsdykdnfgsssfssapyvsndglgsssa pplerrsfignsdiqsldnystasshsggppqpsafsesfpssvagygdiylnagpmlfsgdkdhrfeyshgpiavlans sdpstgpesthplpakmhnynyggnlqenpsgpslmhgqtwtspaqgpgysqgyrghiststgrgrgrglpy (SEQ ID NO:42)

39. Ctk1p human (11) CAC10400
mpsssdtalggggglswaekrleerrkrrrflspqqppllIpllqpqllqppppppplIflaapgtaaaaaaaaaasssc fspgpplevkrlargkrraggrqkrrrgpragqeaekrrvfslpqpqqdggggassgggvtplveyedvssqseqglllg gasaataataaggtggsggspasssgtqrrgegserrprrdrrsssgrskerhrehrrrdgqrggseasksrsrhshsge eraevaksgsssssggrrksasatssssssrkdrdskahrsrtksskeppsaykeppkayredktepkayrrrrslsplg

grddspvshrasqslrsrkspspagggsspysrrlprspspysrrrspsysrhssyerggdvspspysssswrrsrspys
pvlrrsgksrsrspyssrhsrsrsrhrlsrsrsrhssispstltlksslaaelnknkkaraaeaaraaeaakaaeatkaa
eaaakaakasntstptkgntetsasasqtnhvkdvkkikiehapspssggtlkndkaktkpplqvtkvennlivdkatkk
avivgkesksaatkeesvslkektkpltpsigakekeqhvalvtstlpplplppmlpedkeadslrgnisvkavkkevek
klrclladlplppelpggddlskspeekktttqlhskrrpkicgprygetkekdidwgklcvdkfdiigiigegtygqvy
kardkdtgemvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdkedaldfkkdkgafylvfeymdhdlmg
llesglvhfnenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikladfglarlysseesrpytnkvitlwyr
ppelllgeerytpaidvwscgcilgelftkkpifqanqelaqlelisricgspcpavwpdviklpyfntmkpkkqyrrkl
reefvfipaaaldlfdymlaldpskrctaeqalqceflrdvepskmpppdlplwqdchelwskkrrrqkqmgmtddvsti
kaprkdlslglddsrtntpqgvlpssqlksqgssnvapvktgpgqhlnhselaillnllqsktsvnmadfvqvlnikvns
etqqqlnkinlpagilatgekqtdpstpqqesskplggiqpssqtiqpkmetdaaqaavqsafavlltqlikaqqskqkd
vlleerengsgheaslqlrpppepstpvsgqddliqhqdmrileltpepdrprilppdqrppeppepppvteedldyrte
nqhvpttsssltdphagvkaallqllaqhqpqddpkreggidyqagdtyvstsdykdnfgsssfssapyvsndglgsssa
pplerrsfignsdiqsldnystasshsggppqpsafsesfpssvagygdiylnagpmlfsgdkdhrfeyshgpiavlans
sdpstgpesthplpakmhnynyggnlqenpsgpslmhgqtwtspaqgpgysqgyrghiststgrgrgrglpy (SEQ
ID NO:43)

40. Ctk1p human (12) NP_001252
makqydsvecpfcdevskyeklakigqgtfgevfkarhrktgqkvalkkvlmenekegfpitalreikilqllkhenvvn
lieicrtkaspynrckgsiylvfdfcehdlagllsnvlvkftlseikrvmqmllnglyyihrnkilhrdmkaanvlitrd
gvlkladfglarafslaknsqpnrytnrvvtlwyrppelllgerdygppidlwgagcimaemwtrspimqgnteqhqlal
isqlcgsitpevwpnvdnyelyeklelvkgqkrkvkdrlkayvrdpyaldlidkllvldpaqridsddalnhdffwsdpm
psdlkgmlsthltsmfeylapprrkgsqitqqstnqsrnpattnqtefervf (SEQ ID NO:44)

41. Ctk1p human (13) A55262
makqydsvecpfcdevskyeklakigqgtfgevfkarhrktgqkvalkkvlmenekegfpitalreikilqllkhenvvn
lieicrtkaspynrckgsiylvfdfcehdlagllsnvlvkftlseikrvmqmllnglyyihrnkilhrdmkaanvlitrd
gvlkladfglarafslaknsqpnrytnrvvtlwyrppelllgerdygppidlwgagcimaemwtrspimqgnteqhqlal
isqlcgsitpevwpnvdnyelyeklelvkgqkrkvkdrlkayvrdpyaldlidkllvldpaqridsddalnhdffwsdpm
psdlkgmlsthltsmfeylapprrkgsqitqqstnqsrnpattnqtefervf (SEQ ID NO:45)

42. Ctk1p human (14) AAA35668
makqydsvecpfcdevskyeklakigqgtfgevfkarhrktgqkvalkkvlmenekegfpitalreikilqllkhenvvn
lieicrtkaspynrckgsiylvfdfcehdlagllsnvlvkftlseikrvmqmllnglyyihrnkilhrdmkaanvlitrd
gvlkladfglarafslaknsqpnrytnrvvtlwyrppelllgerdygppidlwgagcimaemwtrspimqgnteqhqlal
isqlcgsitpevwpnvdnyelyeklelvkgqkrkvkdrlkayvrdpyaldlidkllvldpaqridsddalnhdffwsdpm
psdlkgmlsthltsmfeylapprrkgsqitqqstnqsrnpattnqtefervf (SEQ ID NO:46)

43. Ctk1p human (15) AAH01968
makqydsvecpfcdevskyeklakigqgtfgevfkarhrktgqkvalkkvlmenekegfpitalreikilqllkhenvvn
lieicrtkaspynrckgsiylvfdfcehdlagllsnvlvkftlseikrvmqmllnglyyihrnkilhrdmkaanvlitrd
gvlkladfglarafslaknsqpnrytnrvvtlwyrppelllgerdygppidlwgagcimaemwtrspimqgnteqhqlal

isqlcgsitpevwpnvdnyelyeklelvkgqkrkvkdrlkayvrdpyaldlidkllvldpaqridsddalnhdffwsdpm psdlkgmlsthltsmfeylapprrkgsqitqqstnqsrnpattnqtefervf (SEQ ID NO:47)

44. Ctk1p human (16) A38282
mknekmkttswlfqshgsteipgrvkkqrkkwvrerraapdrghyvptplpcrpssssrscpstcrpagcrsveefqcl nrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivmnyveh dlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtl wyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtfsehpy nnlrkrfgallsdqgfdlmnkfltyfpgrrlsaqdglkheyfretplpidpsmfptwpakseqqrvkrgtsprppegglg ysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:48)

45. Ctk1p human (17) P50750
makqydsvecpfcdevskyeklakigqgtfgevfkarhrktgqkvalkkvlmenekegfpitalreikilqllkhenvvn lieicrtkaspynrckgsiylvfdfcehdlagllsnvlvkftlseikrvmqmllnglyyihrnkilhrdmkaanvlitrd gvlkladfglarafslaknsqpnrytnrvvtlwyrppelllgerdygppidlwgagcimaemwtrspimqanteqhqlal isqlcgsitpevwpnvdnyelyeklelvkgqkrkvkdrlkayvrdpyaldlidkllvldpaqridsddalnhdffwsdpm psdlkgmlsthltsmfeylapprrkgsqitqqstnqsrnpattnqtefervf (SEQ ID NO:49)

46. Ctk1p human (18) AAA19581
metgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspals pielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqh pnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshag ilkvgdfglareygsplkaytpvvvtlwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdl gtpsekiwpgyselpavkkmtfsrhpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsm fptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:50)

47. Ctk1p human (19) NP_296370
msedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspalspielkqelpkylpalqgcrsve efqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivm nyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytp vvvtlwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtf sehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprpp egglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:51)

48. Ctk1p human (20) AAA36406
msedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspalspielkqelpkylpalqgcrsve efqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivm nyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytp vvvtlwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtf sehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprpp egglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:52)

Figure 4

49. Ctk1p human (21) NP_277026
metgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspals pielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqh pnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshag ilkvgdfglareygsplkaytpvvvtlwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdl gtpsekiwpgyselpavkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsm fptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:53)

50. Ctk1p human (22) AAA19584
mredysdkvkashwsrspprpprerfelgdgrkpvkeekmeerdllsdlqdisdserktssaesssaesgsgseeeeeee eeeeeegstseeseeeeeeeeeetgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevge gtpqssaltegdyvpdspalspielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmek ekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhl hdnwilhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtlwyrapelllgakeystavdmwsvgcifgellt qkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtfsrhpynnlrkrfgallsdqgfdlmnkfltyfpgrris aedglkheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfsl kf (SEQ ID NO:54)

51. Ctk1p human (23) AAC72078
meerdllsdlqdisdserktssaesssaesgsgseeeeeeeeeeeegstseeseeeeeeeeeeeetgsnseeaseqsa eevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspalspielkqelpkylpal qgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnm dkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygs plkaytpvvvtlwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselp avkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsmfptwpakseqqrvkr gtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:55)

52. Ctk1p human (24) NP_277022
meerdllsdlqdisdserktssaesssaesgsgseeeeeeeeeeeeegstseeseeeeeeeeeeeeetgsnseeaseqsa eevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspalspielkqelpkylpal qgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnm dkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygs plkaytpvvvtlwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselp avkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsmfptwpakseqqrvkr gtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:56)

53. Ctk1p human (25) NP_277025
mredysdkvkashwsrspprpprerfelgdgrkpvkeekmeerdllsdlqdisdserktssaesssaesgsgseeeeeee

eeeeeegstseeseeeeeeeeeeeeetgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeee
vgegtpqssaltegdyvpdspalspielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlk
mekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgv
khlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtlwyrapelllgakeystavdmwsvgcifge
lltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgr
risaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpg
fslkf (SEQ ID NO:57)

54. Ctk1p human (26) AAC72082
mredysdkvkashwsrspprpprerfelgdgrkpvkeekmeerdllsdlqdisdserktssaesssaesgsgseeeeeee
eeeeeegstseeseeeeeeeeeeeeetgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeee
vgegtpqssaltegdyvpdspalspielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlk
mekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgv
khlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtlwyrapelllgakeystavdmwsvgcifge
lltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgr
risaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpg
fslkf (SEQ ID NO:58)

55. Ctk1p human (27) AAC83666
mredysdkvkashwsrspprpprerfelgdgrkpvkeekmeerdllsdlqdisdserktssaesssaesgsgseeeeeee
eeeeeegstseeseeeeeeeeeeeeetgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeee
vgegtpqssaltegdyvpdspalspielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlk
mekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgv
khlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtlwyrapelllgakeystavdmwsvgcifge
lltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgr
risaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpg
fslkf (SEQ ID NO:59)

56. Ctk1p human (28) XP_043001
mvalkkvrldnekegfpitaireikilrqlthqsiinmkeivtdkedaldfkkdkgafylvfeymdhdlmgllesglvhf
nenhiksfmrqlmegldychkknflhrdikcsnillnnrgqikladfglarlysseesrpytnkvitlwyrppelllgee
rytpaidvwscgcilgelftkkpifqanqelaqlelisricgspcpavwpdviklpyfntmkpkkqyrrklreefvfipa
aaldlfdymlaldpskrctaeqalqceflrdvepskmpppdlplwqdchelwskkrrqkqmgmtddvstikaprkdlsl
glddsrtntpqgvlpssqlksqgssnvapvktgpgqhlnhselaillnllqsktsvnmadfvqvlnikvnsetqqqlnki
nlpagilatgekqtdpstpqqesskplggiqpssqtiqpkvetdaaqaavqsafavlltqlikaqqskqkdvlleereng
sgheaslqlrpppepstpvsgqddliqhqdmrileltpepdrprilppdqrppeppepppvteedldyrtenqhvpttss
sltdphagvkaallqllaqhqpqddpkreggidyqagdtyvstsdykdnfgsssfssapyvsndglgsssapplerrsfi
gnsdiqsldnystasshsggppqpsafsesfpssvagygdiylnagpmlfsgdkdhrfeyshgpiavlanssdpstgpes
thplpakmhnynyggnlqenpsgpslmhgqtwtspaqgpgysqgyrghiststgrgrgrglpy (SEQ ID NO:60)

57. Ctk1p human (29) A54024
metgsnseeaseqsaeevseeemsedeerenenhflvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspals
pielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqh
pnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshag
ilkvgdfglareygsplkaytpvvltqwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdl

gtpsekiwpgyselpavkkmtgsehpynnlrkrfgallsdqgfdlmnkfltyfpgkrisaedglkheyfretplpidpsm fptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:61)

58. Ctk1p human (30) NP_277069
mknekmkttswlfqshgsteipgrvkkqrkkwgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegf pitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwi lhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplf pgnseidqinkvfkelgtpsekiwpgyselpvvkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedgl kheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:62)

59. Ctk1p human (31) NP_277074
mknekmkttswlfqshgsteipgrvkkqrkkwgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegf pitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwi lhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplf pgnseidqinkvfkelgtpsekiwpgyselpvvkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedgl kheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:63)

60. Ctk1p human (32) AAC72083
mknekmkttswlfqshgsteipgrvkkqrkkwgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegf pitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwi lhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplf pgnseidqinkvfkelgtpsekiwpgyselpvvkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedgl kheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:64)

61. Ctk1p human (33) AAC72088
mknekmkttswlfqshgsteipgrvkkqrkkwgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegf pitslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwi lhrdlktsnlllshagilkvgdfglareygsplkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplf pgnseidqinkvfkelgtpsekiwpgyselpvvkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedgl kheyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:65)

62. Ctk1p human (34) CAA20348
msedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspallpielkqelpkylpalqgcrsve efqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivm nyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytp vvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfpgnseidqinkvfkelgtpsekiwpgyselpvvkkmtf sehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprpp egglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:66)

63. Ctk1p human (35) XP_001532
marehsrrergndgvclfrdrleqlerkrererkmreqqkeqreqkererraeerrkerearrevsahhrtmredysdkv kashwsrspprpprerfelgdgrkpvkeekmeerdllsdlqdisdserktssaesssaesgsgseeeeeeeeeeeegst

seeseeeeeeeeeeeeeetgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqss altegdyvpdspallpielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfp itslreintilkaqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwil hrdlktsnlllshagilkvgdfglareygsplkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfp gnseidqinkvfkelgtpsekiwpgyselpvvkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglk heyfretplpidpsmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:67)

64. Ctk1p human (36) A42823
msedeerenenhlfvvpesrfdrdsgeseeaeeevgegtpqssaltegtyvpdspalspielkqelpkylpalqgcrsve efqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivm nyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytp vvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtf sehpynnlrkrfgallsdqgfdlmnkfltyfpgrrlsaqdglkheyfretplpidpsmfptwpakseqqrvkrgtsprpp egglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:68)

65. Ctk1p human (37) T09568
mknekmkttswlvrtsletefqfqshvsteipgrvrrqrkkwvrerrkssaltegdyvpdslplspielkqelpkylpal qgcrsvdefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnm dkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygs plkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselp avkkmtfsehpynnlrkrfgallseqgfdlmnkfltyfpgrrlsaqdglkheyfretplpidpsmfptwpakseqqrvkr gtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:69)

66. Ctk1p human (38) AAB59449
mknekmkttswlvrtsletefqfqshvsteipgrvrrqrkkwvrerrkssaltegdyvpdslplspielkqelpkylpal qgcrsvdefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnm dkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygs plkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselp avkkmtfsehpynnlrkrfgallseqgfdlmnkfltyfpgrrlsaqdglkheyfretplpidpsmfptwpakseqqrvkr gtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:70)

67. Ctk1p human (39) AAH14464
ereeetgsnseeaseqsaeevseeemsedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdsp allpielkqelpkylpalqgcrsveefqclnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilk aqhpnivtvreivvgsnmdkiyivmnyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnllls hagilkvgdfglareygsplkaytpvvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfpgnseidqinkvf kelgtpsekiwpgyselpvvkkmtfsehpynnlrkrfgallsdqgfdlmnkfltyfpgrrisaedglkheyfretplpid psmfptwpakseqqrvkrgtsprppegglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:71)

68. Ctk1p human (40) AAA19585
msedeerenenhllvvpesrfdrdsgeseeaeeevgegtpqssaltegdyvpdspalspielkqelpkylpalqgcrsvd efqclnrieegtygvvyrakdkktdeivalkrlkmekenegfpitslreintilkaqhpnivtvreivvgsnmdkiyivm nyvehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytp vvvtqwyrapelllgakeystavdmwsvgcifgelltqkplfpgnseidqinkvfkelgtpsekiwpgyselpvvkkmtf srhpynnlrkrfgallseqgfdlmnkfltyfpgrrisaedglkheyfretplpidpsmfptwpakseqqrvkrgtsprpp

egglgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:72)

69. Ctk1p human (41) KP58_HUMAN
mknekmkttswlfqshvsteipgrvrrqrkkwvrerrkssaltegdyvpdslplspielkqelpkylpalqgcrsvdefq
clnrieegtygvvyrakdkktdeivalkrlkmekekegfpitslreintilkaqhpnivtvreivvgsnmdkiyivmnyv
ehdlkslmetmkqpflpgevktlmiqllrgvkhlhdnwilhrdlktsnlllshagilkvgdfglareygsplkaytpvvv
tqwyrapelllgakeystavdmwsvgcifgelltqkplfpgkseidqinkvfkdlgtpsekiwpgyselpavkkmtfseh
pynnlrkrfgallseqgfdlmnkfltyfpgrrlsaqdglkheyfretplpidpsmfptwpakseqqrvkrgtsprppegg
lgysqlgdddlketgfhltttnqgasaagpgfslkf (SEQ ID NO:73)

Dbf2p (5 sequences)

70. Dbf2p human (01) BAA76809
amtagttttfpmsnhtrervtvakltlenfysnlilqheeretrqkklevameeegladeekklrrsqharketeflrlk
rtrlglddfeslkvigrgafgevrlvqkkdtghiyamkilrksdmlekeqvahiraerdilveadgawvvkmfysfqdkr
nlylimeflpggdmmtllmkkdtlteeetqfyisetvlaidaihqlgfihrdikpdnllldakghvklsdfglctglkka
hrtefyrnlthnppsdfsfqnmnskrkaetwkknrrqlaystvgtpdyiapevfmqtgynklcdwwslgvimyemligy
ppfcsetpqetyrkvmnwketlvfppevpisekakdlilrfcidsenrignsgveeikghpffegvdwehirerpaaipie
iksiddtsnfddfpesdilqpvpnttepdykskdwvflnytykrfegltqrgsiptymkagkl (SEQ ID NO:74)

71. Dbf2p human (02) XP_044823
mamtagttttfpmsnhtrervtvakltlenfysnlilqheeretrqkklevameeegladeekklrrsqharketeflrl
krtrlglddfeslkvigrgafgevrlvqkkdtghiyamkilrksdmlekeqvahiraerdilveadgawvvkmfysfqdk
rnlylimeflpggdmmtllmkkdtlteeetqfyisetvlaidaihqlgfihrdikpdnllldakghvklsdfglctglkk
ahrtefyrnlthnppsdfsfqnmnskrkaetwkknrrqlaystvgtpdyiapevfmqtgynklcdwwslgvimyemlig
yppfcsetpqetyrkvmnwketlvfppevpisekakdlilrfcidsenrignsgveeikghpffegvdwehirerpaaipi
eiksiddtsnfddfpesdilqpvpnttepdykskdwvflnytykrfegltqrgsiptymkagkl (SEQ ID NO:75)

72. Dbf2p human (03) NP_009202
mamtgstpcssmsnhtkervtmtkvtlenfysnliaqheeremrqkklekvmeeeglkdeekrlrrsaharketeflrlk
rtrlgledfeslkvigrgafgevrlvqkkdtghvyamkilrkadmlekeqvghiraerdilveadslwvvkmfysfqdkl
nlylimeflpggdmmtllmkkdtlteeetqfyiaetvlaidsihqlgfihrdikpdnllldskghvklsdfglctglkka
hrtefyrnlnhslpsdftfqnmnskrkaetwkrnrrqlafstvgtpdyiapevfmqtgynklcdwwslgvimyemligyp
pfcsetpqetykkvmnwketltfppevpisekakdlilrfccewehrigapgveeiksnsffegvdwehirerpaaisie
iksiddtsnfdefpesdilkptvatsnhpetdyknkdwvfinytykrfegltargaipsymkaak (SEQ ID NO:76)

73. Dbf2p human (04) NP_004681
mkrsekpegyrqmrpktfpasnytvssrqmlqeireslrnlskpsdaakaehnmskmstedprqvrnppkfgthhkalq
eirnsllpfanetnssrstsevnpqmlqdlqaagfdedmviqalqktnnrsieaaiefiskmsyqdprreqmaaaaarpin
asmkpgnvqqsvnrkqswkgskeslvpqrhgpplgesvayhsespnsqtdvgrplsgsgisafvqahpsngqrvnppp
ppqvrsvtpppppprgqtppprgttppppswepnsqtkrysgnmeyvisrispvppgawqegyppppIntspmnppnq
gqrgissvpvgrqpiimqsssskfnfpsgrpgmqngtgqtdfmihqnvvpagtvnrqppppyplTaangqspsalqtggsa
apssytngsipqsmmvpnrnshnmelynisvpglqtnwpqsssapaqssps sgheiptwqpnipvrsnsfnnplgnras
hsansqpsattvtaitpapiqqpvksmrvlkpelqtalapthpswipqpiqtvqpspfpegtasnvtvmppvaeapnyqgp
pppypkhllhqnpsvppyesiskpskedqpslpkedeseksyenvdsgdkekkqittspitvrknkkdeerresriqsysp
qafkffmeqhvenvlkshqqrlhrkkqlenemmrvglsqdaqdqmrkmlcqkesnyirllkrakmdksmfvkiktlgig

afgevclarkvdtkalyatktlrkkdvllrnqvahvkaerdilaeadnewvvrlyysfqdkdnlyfvmdyipggdmmslli rmgifpeslarfyiaeltcavesvhkmgfihrdikpdnilidrdghikltdfglctgfrwthdskyyqsgdhprqdsmdfsne wgdpsscrcgdrlkplerraarqhqrclahslvgtpnyiapevllrtgytqlcdwwsvgvilfemlvgqppflaqtpletqm kvinwqtslhippqaklspeasdliiklcrgpedrlgkngadeikahpffktidfssdlrqqsasyipkithptdtsnfd pvdpdklwsddneeenvndtlngwykngkhpehafyeftfrrffddngypynypkpieyeyinsqgseqqsdeddqnt gseikmrdlvyv (SEQ ID NO:77)

74. Dbf2p human (05) BAA92381
nsdtsldakvlgskdatsskqqmratpkfgpyqkalreirysllpfanesgtsaaaevnrqmlqelvnagcdqemagral kqtgsrsieaaleyiskmgyldprneqivrvikqtspgkglmptpvtrrpsfegtgdsfasyhqlsgtpyegpsfgadgp taleemprpyvdylfpgvgphgpghqhqhppkgygasveaagahfplqgahygrphllvpgeplgygvqrspsfqsktp petggyaslptkgqggppgaglafpppaaglyvphphhkqagpvahqlhvlgsrsqvfasdsppqslltpsrnslnvdlye lsstsvqqwpaatlarrdslqkpgleapprahvafrpdcpvpsrtnsfnshqprpgppgkaepslpapntvtavsaahil hpvksvrvlrpepqtavgpshpawvpapapapapapaaegldakeehalalggagafpldveyggpdrsarlrptrst cccakseqydldslcagmeqslragpnepeggdksrksakgdkggkdkkqiqtspvpvrknsrdeekresriksyspyaf kffmeqhvenviktyqqkvnrrlqleqemakaglceaeqeqmrkilyqkesnynrlkrakmdksmfvkiktlgigafge vclackvdthalyamktlrkkdvlnrnqvahvkaerdilaeadnewvvklyysfqdkdslyfvmdyipggdmmsllirm evfpehlarfyiaeltlaiesvhkmgfihrdikpdnilidldghikltdfglctgfrwthnskyyqkgshvrqdsmepsdlw ddvsncrcgdrlktleqrarkqhqrslahslvgtpnyiapevllrkgytqlcdwwsvgvilfemlvgqppflaptptetq lkvinwentlhipaqvklspeardlitklccsadhrlgrngaddlkahpffsaidfssdirkqpapyvptishpmdtsnf dpvdeespwndasegstkawdtltspnnkhpehafyeftfrrffddngypfrcpkpsgaeasqaessdlessdlvdqteg cqpvyv (SEQ ID NO:78)

Dbp3p (19 sequences)

75. Dbp3p human (01) NP_006377
mrgggfgdrdrdrdrggfgargggglppkkfgnpgerlrkkkwdlselpkfeknfyvehpevarltpyevdelrrkkeit vrggdvcpkpvfafhhanfpqyvmdvlmdqhfteptpiqcqgfplalsgrdmvgiaqtgsgktlayllpaivhinhqpyl ergdgpiclvlaptrelaqqvqqvaddygkcsrlkstciyggapkgpqirdlergveiciatpgrlidflesgktnlrrc tylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflrdytqinvgnlelsanhnilqivdvcme sekdhkliqlmeeimaekenktiifvetkrrcddltrrmrrdgwpamcihgdksqperdwvlnefrsgkapiliatdvas rgldvedvkfvinydypnssedyvhrigrtarstnkgtaytfftpgnlkqarelikvleeanqainpklmqlvdhrgggg ggggrsryrttssannpnlmyqdecdrrlrgvkdggrrdsasyrdrsetdragyangsgygspnsafgaqagqytygqgt ygaaaygtssytaqeygagtygassttstgrssqsssqqfsgigrsgqqpqplmsqqfaqppgatnmigymgqtayqypp pppppppsrk (SEQ ID NO:79)

76. Dbp3p human (02) Q92841
mrgggfgdrdrdrdrggfgargggglppkkfgnpgerlrkkkwdlselpkfeknfyvehpevarltpyevdelrrkkeit vrggdvcpkpvfafhhanfpqyvmdvlmdqhfteptpiqcqgfplalsgrdmvgiaqtgsgktlayllpaivhinhqpyl ergdgpiclvlaptrelaqqvqqvaddygkcsrlkstciyggapkgpqirdlergveiciatpgrlidflesgktnlrrc tylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflrdytqinvgnlelsanhnilqivdvcme sekdhkliqlmeeimaekenktiifvetkrrcddltrrmrrdgwpamcihgdksqperdwvlnefrsgkapiliatdvas rgldvedvkfvinydypnssedyvhrigrtarstnkgtaytfftpgnlkqarelikvleeanqainpklmqlvdhrgggg ggggrsryrttssannpnlmyqdecdrrlrgvkdggrrdsasyrdrsetdragyangsgygspnsafgaqagqytygqgt ygaaaygtssytaqeygagtygassttstgrssqsssqqfsgigrsgqqpqplmsqqfaqppgatnmigymgqtayqypp pppppppsrk (SEQ ID NO:80)

77. Dbp3p human (03) S72367
mrgggfgdrdrdrdrggfgargggglppkkfgnpgerlrkkkwdlselpkfeknfyvehpevarltpyevdelrrkkeit
vrggdvcpkpvfafhhanfpqyvmdvlmdqhfteptpiqcqgfplalsgrdmvgiaqtgsgktlayllpaivhinhqpyl
ergdgpiclvlaptrelaqqvqqvaddygkcsrlkstciyggapkgpqirdlergveiciatpgrlidflesgktnlrrc
tylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflrdytqinvgnlelsanhnilqivdvcme
sekdhkliqlmeeimaekenktiifvetkrrcddltrrmrrdgwpamcihgdksqperdwvlnefrsgkapiliatdvas
rgldvedvkfvinydypnssedyvhrigrtarstnkgtaytfftpgnlkqarelikvleeanqainpklmqlvdhrgggg
ggggrsryrttssannpnlmyqdecdrrlrgvkdggrrdsasyrdrsetdragyangsgygspnsafgaqagqytygqgt
ygaaaygtssytaqeygagtygassttstgrssqsssqqfsgigrsgqqpqplmsqqfaqppgatnmigymgqtayqypp
pppppppsrk (SEQ ID NO:81)

78. Dbp3p human (04) AAC50787
mrgggfgdrdrdrdrggfgargggglppkkfgnpgerlrkkkwdlselpkfeknfyvehpevarltpyevdelrrkkeit
vrggdvcpkpvfafhhanfpqyvmdvlmdqhfteptpiqcqgfplalsgrdmvgiaqtgsgktlayllpaivhinhqpyl
ergdgpiclvlaptrelaqqvqqvaddygkcsrlkstciyggapkgpqirdlergveiciatpgrlidflesgktnlrrc
tylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflrdytqinvgnlelsanhnilqivdvcme
sekdhkliqlmeeimaekenktiifvetkrrcddltrrmrrdgwpamcihgdksqperdwvlnefrsgkapiliatdvas
rgldvedvkfvinydypnssedyvhrigrtarstnkgtaytfftpgnlkqarelikvleeanqainpklmqlvdhrgggg
ggggrsryrttssannpnlmyqdecdrrlrgvkdggrrdsasyrdrsetdragyangsgygspnsafgaqagqytygqgt
ygaaaygtssytaqeygagtygassttstgrssqsssqqfsgigrsgqqpqplmsqqfaqppgatnmigymgqtayqypp
pppppppsrk (SEQ ID NO:82)

79. Dbp3p human (05) CAB09792
mrgggfgdrdrdrdrggfgargggglppkkfgnpgerlrkkkwdlselpkfeknfyvehpevarltpyevdelrrkkeit
vrggdvcpkpvfafhhanfpqyvmdvlmdqhfteptpiqcqgfplalsgrdmvgiaqtgsgktlayllpaivhinhqpyl
ergdgpiclvlaptrelaqqvqqvaddygkcsrlkstciyggapkgpqirdlergveiciatpgrlidflesgktnlrrc
tylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflrdytqinvgnlelsanhnilqivdvcme
sekdhkliqlmeeimaekenktiifvetkrrcddltrrmrrdgwpamcihgdksqperdwvlnefrsgkapiliatdvas
rgldvedvkfvinydypnssedyvhrigrtarstnkgtaytfftpgnlkqarelikvleeanqainpklmqlvdhrgggg
ggggrsryrttssannpnlmyqdecdrrlrgvkdggrrdsasyrdrsetdragyangsgygspnsafgaqagqytygqgt
ygaaaygtssytaqeygagtygassttstgrssqsssqqfsgigrsgqqpqplmsqqfaqppgatnmigymgqtayqypp
pppppppsrk (SEQ ID NO:83)

80. Dbp3p human (06) AAH00595
mrgggfgdrdrdrdrggfgargggglppkkfgnpgerlrkkkwdlselpkfeknfyvehpevarltpyevdelrrkkeit
vrggdvcpkpvfafhhanfpqyvmdvlmdqhfteptpiqcqgfplalsgrdmvgiaqtgsgktlayllpaivhinhqpyl
ergdgpiclvlaptrelaqqvqqvaddygkcsrlkstciyggapkgpqirdlergveiciatpgrlidflesgktnlrrc
tylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflrdytqinvgnlelsanhnilqivdvcme
sekdhkliqlmeeimaekenktiifvetkrrcddltrrmrrdgwpamcihgdksqperdwvlnefrsgkapiliatdvas
rgldvedvkfvinydypnssedyvhrigrtarstnkgtaytfftpgnlkqarelikvleeanqainpklmqlvdhrgggg
ggggrsryrttssannpnlmyqdecdrrlrgvkdggrrdsasyrdrsetdragyangsgygspnsafgaqagqytygqgt
ygaaaygtssytaqeygagtygassttstgrssqsssqqfsgigrsgqqpqplmsqqfaqppgatnmigymgqtayqypp
pppppppsrk (SEQ ID NO:84)

81. Dbp3p human (07) 226021

fggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrskeitvrghncpkpvlnfyean
fpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqpflergdgpiclvlaptrela
qqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlrrttylvldeadrmldmgfep
qirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvchdvekdeklirlmeeimsek
enktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdvasrgldvedvkfvinydypn
ssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgsgrsrgrggmkddrrdrysag
krggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrtgnptgtyqngydstqqygsn
vpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:85)

82. Dbp3p human (08) NP_004387
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:86)

83. Dbp3p human (09) XP_008344
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:87)

84. Dbp3p human (10) P17844
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:88)

85. Dbp3p human (11) JC1087
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs

grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:89)

86. Dbp3p human (12) CAA36324
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:90)

87. Dbp3p human (13) CAA33751
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:91)

88. Dbp3p human (14) AAB84094
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:92)

89. Dbp3p human (15) AAH16027
msgyssdrdrgrdrgfgaprfggsragplsgkkfgnpgeklvkkkwnldelpkfeknfyqehpdlarrtaqevetyrrsk
eitvrghncpkpvlnfyeanfpanvmdviarqnfteptaiqaqgwpvalsgldmvgvaqtgsgktlsyllpaivhinhqp
flergdgpiclvlaptrelaqqvqqvaaeycracrlkstciyggapkgpqirdlergveiciatpgrlidflecgktnlr
rttylvldeadrmldmgfepqirkivdqirpdrqtlmwsatwpkevrqlaedflkdyihinigalelsanhnilqivdvc
hdvekdeklirlmeeimsekenktivfvetkrrcdeltrkmrrdgwpamgihgdksqqerdwvlnefkhgkapiliatdv
asrgldvedvkfvinydypnssedyihrigrtarstktgtaytfftpnnikqvsdlisvlreanqainpkllqlvedrgs
grsrgrggmkddrrdrysagkrggfntfrdrenydrgyssllkrdfgaktqngvysaanytngsfgsnfvsagiqtsfrt
gnptgtyqngydstqqygsnvpnmhngmnqqayaypataaapmigypmptgysq (SEQ ID NO:93)

90. Dbp3p human (16) NP_061135
mshhggapkastwvvasrrsstvsraperrpaeelnrtgpegysvgrggrwrgtsrppeavaagheelplcfalkshfvg
avigrggskikniqsttnttiqiiqeqpeslvkifgskamqtkakavidnfvkkleenynsecgidtafqpsvgkdgstd

nnvvagdrplidwdqireeglkwqktkwadlppikknfykestatsamskveadswrkenfnitwddlkdgekrpipnp
tctfddafqcypevmenikkagfqkptpiqsqawpivlqgidligvaqtgtgktlcylmpgfihlvlqpslkgqrnrpgml
vltptrelalqvegecckysykglrsvcvygggnrdeqieelkkgvdiiiatpgrlndlqmsnfvnlknitylvldeadk
mldmgfepqimkilldvrpdrqtvmtsatwphsvhrlaqsylkepmivyvgtldlvavssvkqniivtteeekwshmqtf
lqsmsstdkvivfvsrkavadhlssdlilgnisveslhgdreqrdrekalenfktgkvriliatdlasrgldvhdvthvy
nfdfprnieeyvhrigrtgragrtgvsittltrndwrvaselinileranqsipeelvsmaerfeahqrkremerkmerp
qgrpkkfh (SEQ ID NO:94)

91. Dbp3p human (17) CAB92442
mshhggapkastwvvasrrsstvsraperrpaeelnrtgpegysvgrggrwrgtsrppeavaagheelplcfalkshfvg
avigrggskikniqsttnttiqiiqeqpeslvkifgskamqtkakavidnfvkkleenynsecgidtafqpsvgkdgstd
nnvvagdrplidwdqireeglkwqktkwadlppikknfykestatsamskveadswrkenfnitwddlkdgekrpipnp
tctfddafqcypevmenikkagfqkptpiqsqawpivlqgidligvaqtgtgktlcylmpgfihlvlqpslkgqrnrpgml
vltptrelalqvegecckysykglrsvcvygggnrdeqieelkkgvdiiiatpgrlndlqmsnfvnlknitylvldeadk
mldmgfepqimkilldvrpdrqtvmtsatwphsvhrlaqsylkepmivyvgtldlvavssvkqniivtteeekwshmqtf
lqsmsstdkvivfvsrkavadhlssdlilgnisveslhgdreqrdrekalenfktgkvriliatdlasrgldvhdvthvy
nfdfprnieeyvhrigrtgragrtgvsittltrndwrvaselinileranqsipeelvsmaerfeahqrkremerkmerp
qgrpkkfh (SEQ ID NO:95)

92. Dbp3p human (18) CAB66685
mshhggapkastwvvasrrsstvsraperrpaeelnrtgpegysvgrggrwrgtsrppeavaagheelplcfalkshfvg
avigrggskikniqsttnttiqiiqeqpeslvkifgskamqtkakavidnfvkkleenynsecgidtafqpsvgkdgstd
nnvvagdrplidwdqireeglkwqktkwadlppikknfykestatsamskveadswrkenfnitwddlkdgekrpipnp
tctfddafqcypevmenikkagfqkptpiqsqawpivlqgidligvaqtgtgktlcylmpgfihlvlqpslkgqrnrpgml
vltptrelalqvegecckysykglrsvcvygggnrdeqieelkkgvdiiiatpgrlndlqmsnfvnlknitylvldeadk
mldmgfepqimkilldvrpdrqtvmtsatwphsvhrlaqsylkepmivyvgtldlvavssvkqniivtteeekwshmqtf
lqsmsstdkvivfvsrkavadhlssdlilgnisveslhgdreqrdrekalenfktgkvriliatdlasrgldvhdvthvy
nfdfprnieeyvhrigrtgragrtgvsittltrndwrvaselinileranqsipeelvsmaerfeahqrkremerkmerp
qgrpkkfh (SEQ ID NO:96)

93. Dbp3p human (19) XP_004395
mshhggapkastwvvasrrsstvsraperrpaeelnrtgpegysvgrggrwrgtsrppeavaagheelplcfalkshfvg
avigrggskikniqsttnttiqiiqeqpeslvkifgskamqtkakavidnfvkkleenynsecgidtafqpsvgkdgstd
nnvvagdrplidwdqireeglkwqktkwadlppikknfykestatsamskveadswrkenfnitwddlkdgekrpipnp
tctfddafqcypevmenikkagfqkptpiqsqawpivlqgidligvaqtgtgktlcylmpgfihlvlqpslkgqrnrpgml
vltptrelalqvegecckysykglrsvcvygggnrdeqieelkkgvdiiiatpgrlndlqmsnfvnlknitylvldeadk
mldmgfepqimkilldvrpdrqtvmtsatwphsvhrlaqsylkepmivyvgtldlvavssvkqniivtteeekwshmqtf
lqsmsstdkvivfvsrkavadhlssdlilgnisveslhgdreqrdrekalenfktgkvriliatdlasrgldvhdvthvy
nfdfprnieeyvhrigrtgragrtgvsittltrndwrvaselinileranqsipeelvsmaerfkahqqkremerkmerp
qgrpkkfh (SEQ ID NO:97)

Dbr1p (4 sequences)

94. Dbr1p human (01) NP_057300
mrvavagcchgeldkiyetlalaerrgpgpvdlllccgdfqavrneadlrcmavppkyrhmqtfyryysgekkapvltlf
iggnheasnhlqelpyggwvapniyylglagvvkyrgvriggisgifkshdyrkghfecppynsstirsiyhvrnievyk

lkqlkqpidiflshdwprsiyhygnkkqllktksffrqevenntlgspaasellehlkptywfsahlhvkfaalmqhqak
dkgqtaratkflaldkclphrdflqileiehdpsapdyleydiewltilratddlinvtgrlwnmpennglharwdysat
eegmkevleklnhdlkvpcnfsvtaacydpskpqtqmqlihrinpqttefcaqlgiidinvrlqkskeehhvcgeyeeqd
dvesndsgedqseyntdtsalssinpdeimldeeededsivsahsgmnttigrsllikllsfcsfsdvrilpgsmivssd
dtvdstidregkpgglvesgngedltkvplkrlsdehepeqrkkikrrnqaiyaavddddddaa

95. Dbr1p human (02) AAD53327
mrvavagcchgeldkiyetlalaerrgpgpvdlllccgdfqavrneadlrcmavppkyrhmqtfyryysgekkapvltlf
iggnheasnhlqelpyggwvapniyylglagvvkyrgvriggisgifkshdyrkghfecppynsstirsiyhvrnievyk
lkqlkqpidiflshdwprsiyhygnkkqllktksffrqevenntlgspaasellehlkptywfsahlhvkfaalmqhqak
dkgqtaratkflaldkclphrdflqileiehdpsapdyleydiewltilratddlinvtgrlwnmpennglharwdysat
eegmkevleklnhdlkvpcnfsvtaacydpskpqtqmqlihrinpqttefcaqlgiidinvrlqkskeehhvcgeyeeqd
dvesndsgedqseyntdtsalssinpdeimldeeededsivsahsgmnttigrsllikllsfcsfsdvrilpgsmivssd
dtvdstidregkpgglvesgngedltkvplkrlsdehepeqrkkikrrnqaiyaavddddddaa

96. Dbr1p human (03) XP_051602
mrvavagcchgeldkiyetlalaerrgpgpvdlllccgdfqavrneadlrcmavppkyrhmqtfyryysgekkapvltlf
iggnheasnhlqelpyggwvapniyylglagvvkyrgvriggisgifkshdyrkghfecppynsstirsiyhvrnievyk
lkqlkqpidiflshdwprsiyhygnkkqllktksffrqevenntlgspaasellehlkptywfsahlhvkfaalmqhqak
dkgqtaratkflaldkclphrdflqileiehdpsapdyleydiewltilratddlinvtgrlwnmpennglharwdysat
eegmkevleklnhdlkvpcnfsvtaacydpskpqtqmqlihrinpqttefcaqlgiidinvrlqkskeehhvcgeyeeqd
dvesndsgedqseyntdtsalssinpdeimldeeededsivsahsgmntpsvepsdqasefsasfsdvrilpgsmivssd
dtvdstidregkpggtvesgngedltkvplkrlsdehepeqrkkikrrnqaiyaavddddddaa

97. Dbr1p human (04) AAH09472
mrvavagcchgeldkiyetlalaerrgpgpvdlllccgdfqavrneadlrcmavppkyrhmqtfyryysgekkapvltlf
iggnheasnhlqelpyggwvapniyylglagvvkyrgvriggisgifkshdyrkghfecppynsstirsiyhvrnievyk
lkqlkqpidiflshdwprsiyhygnkkqllktksffrqevenntlgspaasellehlkptywfsahlhvkfaalmqhqak
dkgqtaratkflaldkclphrdflqileiehdpsapdyleydiewltilratddlinvtgrlwnmpennglharwdysat
eegmkevleklnhdlkvpcnfsvtaacydpskpqtqmqlihrinpqttefcaqlgiidinvrlqkskeehhvcgeyeeqd
dvesndsgedqseyntdtsalssinpdeimldeeededsivsahsgmntpsvepsdqasefsasfsdvrilpgsmivssd
dtvdstidregkpggtvesgngedltkvplkrlsdehepeqrkkikrrnqaiyaavddddddaa

Doa4p (14 sequences)

98. Doa4p human (01) NP_005145
mpavasvpkelylsssIkdlnkktevkpekistksyvhsalkifktaeecrldrdeerayvlymkyvtvynlikkrpdfk
qqqdyfhsilgpgnikkaveeaerlseslklryeeaevrkkleekdrqeeaqrlqqkrqetgredggtlakgslenvlds
kdktqksngeknekcetkekgaitakelytmmtdknisliimdarrmqdyqdscilhslsvpeeaispgvtaswieahlp
ddskdtwkkrgnveyvvlldwfssakdlqigttlrslkdalfkwesktvlrneplvleggyenwllcypqyttnakvtpp
prrqneevsisldftypsleesipskpaaqtppasievdenielisgqnerlngplnistpvepvaasksdvspiiqpvps
iknvpqidrtkkpavklpeehriksestnheqqspqsgkvipdrstkpvvfsptlmltdeekarihaetallmeknkqek
elrerqqeeqkeklrkeeqeqkakkkqeaeeneitekqqkakeemekkeseqakkedketsakrgkeitgvkrqsksehe
tsdakksvedrgkrcptpeiqkkstgdvphtsvtgdsgsgkpfkikgqpesgilrtgtfredtddternkaqrepltrar
seemgrivpglpsgwakfldpitgtfryyhsptntvhmyppemapssappstppthkakpqipaerdrepsklkrsyssp
ditqaiqeeekrkptvtptvnrenkptcypkaeisrlsasqirnlnpvfggsgpaltglrnlgntcymnsilqclcnaph

ladyfnrncyqddinrsnllghkgevaeefgiimkalwtgqyryispkdfkitigkindqfagysqqdsqelllflmdgl
hedlnkadnrkrykeenndhlddfkaaehawqkhkqlnesiivalfqgqfkstvqcltchkksrtfeafmylslplasts
kctlqdclrlfskeekltdnnrfycshcrarrdslkkieiwklppvllvhlkrfsydgrwkqklqtsvdfplenldlsqy
vigpknnlkkynlfsvsnhyggldgghytaycknaarqrwfkfddhevsdisvssvkssaayilfytslgprvtdvat

99. Doa4p human (02) NP_036607
mpqasehrlgrtreppvniqprvgsklpfaprarskermpasgpnpmlrplpprpglpderlkklelgrgrtsgprprg
plradhgvplpgsppptvalplpsrtnlarsksvssgdlrpmgialgghrgtgelgaalsrlalrpepptlrrstslrrl
ggfpgpptlfsirteppashgsfhmisarssepfysddkmahhtlllgsghvglrnlgntcflnavlqclsstrplrdfc
lrrdfrqevpgggraqelteafadvigalwhpdsceavnptrfravfqkyvpsfsgysqqdaqeflkllmerlhleinrr
grrappilangpvpspprrggalleepelsdddranlmwkryleredskivdlfvgqlksclkcqacgyrsttfevfcdl
slpipkkgfaggkvslrdcfnlftkeeelesenapvcdrcrqktrstkkltvqrfprilvlhlnrfsasrgsikkssvgv
dfplqrlslgdfasdkagspvyqlyalcnhsgsvhyghytalcrcqtgwhvyndsrvspvsenqvassegyvlfyqlmqe
pprcl

100. Doa4p human (03) AAH03130
misarssepfysddkmahhtlllgsghvglrnlgntcflnavlqclsstrplrdfclrrdfrqevpgggraqelteafad
vigalwhpdsceavnptrfravfqkyvpsfsgysqqdaqeflkllmerlhleinrrgrrappilangpvpspprrggall
eepelsdddranlmwkryleredskivdlfvgqlksclkcqacgyrsttfevfcdlslpipkkgfaggkvslrdcfnlft
keeelesenapvcdrcrqktrstkkltvqrfprilvlhlnrfsasrgsikkssvgvdfplqrlslgdfasdkagspvyql
yalcnhsgsvhyghytalcrcqtgwhvyndsrvspvsenqvassegyvlfyqlmqepprcl

101. Doa4p human (04) NP_057656
misarssepfysddkmahhtlllgsghvglrnlgntcflnavlqclsstrplrdfclrrdfrqevpgggraqelteafad
vigalwhldsceavnptrfravfqkyvpsfsgysqqdaqeflkllmerlhleinrrgrrappilangpvpspprrggall
eepelsdddranlmwkryleredskivdlfvgqlksclkcqacgyrsttfevfcdlslpipkkgfaggkvflrdcfnlft
keeelesenapvcdrcrqktrstkkltvqrfprilvlhlnrfsasrgsikkssvgvdfplqrlslgdfasdkagspvyql
yalcnhsgsvhyghytalcrcqtgwhvyndsrvspvsenqvassegyvlfyqlmqepprcl

102. Doa4p human (05) XP_051386
msqlsstlkrytesarytdahyaksgygaytpssyganlaasllekeklgfkpvptssfltrprtygpsslldydrgrpl
lrpditgggkraesqtrgterplgsglsggsgfpygvtnnclsylpinaydqgvtltqkldsqsdlardfsslrtsdsyr
idprnlgrspmlartrkelctlqglyqtascpeylvdylenygrkgsasqvpsqappsrvpeiisptyrpigrytlwetg
kgqapgpsrssspgrdgmnsksaqglaglrnlgntcfmnsilqclsntrelrdyclqrlymrdlhhgsnahtalveefak
liqtiwtsspndvvspsefktqiqryaprfvgynqqdaqeflrflldglhnevnrvtlrpksnpenldhlpddekgrqmw
rkyleredsrigdlfvgqlkssltctdcgycstvfdpfwdlslpiakrgypevtlmdcmrlftkedvldgdekptccrcr
grkrcikkfsiqrfpkilvlhlkrfsesrirtskltfvnfplrdldlrefasentnhavynlyavsnhsgttmgghyta
ycrspgtgewhtfndssvtpmsssqvrtsdayllfyelasppsrm

103. Doa4p human (06) BAB71388
msqlsstlkrytesarytdahyaksgygaytpssyganlaasllekeklgfkpvptssfltrprtygpsslldydrgrpl
lrpditgggkraesqtrgterplgsglsggsgfpygvtnnclsylpinaydqgvtltqkldsqsdlardfsslrtsdsyr
idprnlgrspmlartrkelctlqglyqtascpeylvdylenygrkgsasqvpsqappsrvpeiisptyrpigrytlwetg
kgqapgpsrssspgrdgmnsksaqglaglrnlgntcfmnsilqclsntrelrdyclqrlymrdlhhgsnahtalveefak
liqtiwtsspndvvspsefktqiqryaprfvgynqqdaqeflrflldglhnevnrvtlrpksnpenldhlpddekgrqmw
rkyleredsrigdlfvgqlkgsltctdcgycstvfdpfwdlslpiakrgypevtlmdcmrlftkedvldgdekptccrcr

grkrcikkfsiqrfpkilvlrlkrfsesrirtsklttfvnfplrdldlrefasentnhavynlyavsnhsgttmgghyta
ycrspgtgewhtfndssvtpmsssqvrtsdayllfyelasppsrm

104. Doa4p human (07) AAC28392
mlnkaknsksaqglaglrnlgntcfmnsilqclsntrelrdyclqrlymrdlhhgsnahtalveefakliqtiwtsspnd
vvspsefktqiqryaprfvgynqqdaqeflrflldglhnevnrvtlrpksnpenldhlpddekgrqmwrkyleredsrig
dlfvgqlkssltctdcgycstvfdpfwdlslpiakrgypevtlmdcmrlftkedvldgdekptccrcrgrkrcikkfsiq
rfpkilvlhlkrfsesrirtsklttfvnfplrdldlrefasentnhavynlyavsnhsgttmgghytaycrspgtgewht
fndssvtpmsssqvrtsdaylhfyelasptspi

105. Doa4p human (08) AAG17222
mpqasehrlgrtreppvniqprvgsklpfaprarskerrnpasgpnpmlrplpprpglpderlkklelgrgrtsgprprg
plradhgvplpgspppptvalplpsrtnlarsksvssgdlrpmgialgghrgtgelgaalsrlalrpepptlrrstslrrl
ggfpgpptlfsirteppashgsfhmisagplslstlmtrwlithsfwalvmlaskpgkhvlpeccaeclsstrplrdfcl
rrdfrqevpgggraqelteafadvigalwhpdsceavnptrfravfqkyvpsfsgysqqdaqeflkllmerlhleinrrg
rrappilangpvpspprrggalleepelsdddranlmwkryleredskivdlfvgqlksclkcqacgyrsttfevfcdls
lpipkkgfaggkvslrdcfnlftkeeelesenapvcdrcrqktrstkkltvqrfprilvlhlnrfsasrgsikkssvgvd
fplqrlslgdfasdkagsvhyghytalcrcqtgwhvyndsrvspvsenqvassegyvlfyqlmqepprcl

106. Doa4p human (09) NP_006304
maeggaadldtqrsdiatllktslrkgdtwylvdsrwfkqwkkyvgfdswdkyqmgdqnvypgpidnsgllkdgdaqsl
kehlideldyillptegwnklvswytlmegqepiarkvveqgmfvkhckvevyltelklcengnmnnvvtrrfskadtidt
iekeirkifsipdeketrlwnkymsntfeplnkpdstiqdaglyqgqvlvieqknedgtwprgpstpnvknsnyclpsyt
ayknydysepgrnneqpglcglsnlgntcfmnsaiqclsntppltey flndkyqeelnfdnplgmrgeiaksyaelikqm
wsgkfsyvtprafktqvgrfapqfsgyqqqdcqellaflldglhedlnrirkkpyiqlkdadgrpdkvvaeeawenhlkr
ndsiivdifhglfkstlvcpecakisvtfdpfcyltlplpmkkertlevylvrmdpltkpmqykvvvpkignildlctal
salsgipadkmivtdiynhrfhrifamdenlssimerddiyvfeininrtedtehviipvclrekfrhssythhtgsslf
gqpflmavprnntedklynllllrmcryvkisteteetegslhcckdqningngpngiheegspsemetdepddessqdq
elpsenensqsedsvggdndsenglctedtckgqltghkkrlftfqfnnlgntdinyikddtrhirfddrqlrldersfl
aldwdpdlkkryfdenaaedfekhesveykppkkpfvklkdcielfttkeklgaedpwycpnckehqqatkkldlwslpp
vlvvhlkrfsysrymrdkldtlvdfpindldmseflinpnagpcrynliavsnhyggmggghytafaknkddgkwyyfd
dssvstasedqivskaayvlfyqrqdtfsgtgffpldretkgasaatgiplesdedsndndndienencmhtn

107. Doa4p human (10) BAA25455
ggaadldtqrsdiatllktslrkgdtwylvdsrwfkqwkkyvgfdswdkyqmgdqnvypgpidnsgllkdgdaqslkeh
lideldyillptegwnklvswytlmegqepiarkvveqgmfvkhckvevyltelklcengnmnnvvtrrfskadtidtiek
eirkifsipdeketrlwnkymsntfeplnkpdstiqdaglyqgqvlvieqknedgtwprgpstpnvknsnyclpsytayk
nydysepgrnneqpglcglsnlgntcfmnsaiqclsntppltey flndkyqeelnfdnplgmrgeiaksyaelikqmwsg
kfsyvtprafktqvgrfapqfsgyqqqdcqellaflldglhedlnrirkkpyiqlkdadgrpdkvvaeeawenhlkrnds
iivdifhglfkstlvcpecakisvtfdpfcyltlplpmkkertlevylvrmdpltkpmqykvvvpkignildlctalsal
sgipadkmivtdiynhrfhrifamdenlssimerddiyvfeininrtedtehviipvclrekfrhssythhtgsslfgqp
flmavprnntedklynllllrmcryvkisteteetegslhcckdqningngpngiheegspsemetdepddessqdqelp
senensqsedsvggdndsenglctedtckgqltghkkrlftfqfnnlgntdinyikddtrhirfddrqlrldersflald
wdpdlkkryfdenaaedfekhesveykppkkpfvklkdcielfttkeklgaedpwycpnckehqqatkkldlwslppvl
vvhlkrfsysrymrdkldtlvdfpindldmseflinpnagpcrynliavsnhyggmggghytafaknkddgkwyyfdds
svstasedqivskaayvlfyqrqdtfsgtgffpldretkgasaatgiplesdedsndndndienencmhtn

108. Doa4p human (11) Q9Y4E8
mgdqnvypgpidnsgllkdgdaqslkehlideldyillptegwnklvswytlmegqepiarkvveqgmfvkhckvevyl
telklcengnmnnvvtrrfskadtidtiekeirkifsipdeketrlwnkymisntfeplnkpdstiqdaglyqgqvlvieqk
neqknedgtwprgpstpnvknsnyclpsytayknydysepgrnneqpglcglsnlgntcfmnsaiqclsntpplteyfln
dkyqeelnfdnplgmrgeiaksyaelikqmwsgkfsyvtprafktqvgrfapqfsgyqqqdcqellaflldglhedlnri
rkkpyiqlkdadgrpdkvvaeeawenhlkrndsiivdifhglfkstlvcpecakisvtfdpfcyltlplpmkkertlevy
lvrmdpltkpmqykvvvpkignildlctalsalsgipadkmivtdiynhrfhrifamdenlssimerddiyvfeininra
edtehviipvclrekfrhssythhtgsslfgqpflmavprnntedklynlllrmcryvkisteteetegslhcckdqni
ngngpngiheegspsemetdepddessqdqelpsenensqsedsvggdndsenglctedtckgqltghkkrlftfqfnnl
gntdinyikddtrhirfddrqlrldersflaldwdpdlkkryfdenaaedfekhesveykppkkpfvklkdcielfttke
klgaedpwycpnckehqqatkkldlwslppvlvvhlkrfsysrymrdkldtlvdfpindldmseflinpnagpcrynlia
vsnhyggmggghytafaknkddgkwyyfddssvstasedqivskaayvlfyqrqdtfsgtgffpldretkgasaatgipl
esdedsndhdndienencmhtn

109. Doa4p human (12) O94966
agcgglarlsvpcwriwpqraakiagpgrkrrspdpdavadpgalwlstkrlkmsggasatgprrgppgledttskkkqk
dranqeskdgdprketgsryvaqagleplasgdpsasashaagitgsrhrtrlffpsssgsastpqeeqtkegacedphd
llatptpellldwrqsaeevivklrvgvgplqledvdaaftdtdcvvrfaggqqwggvfyaeiksscakvqtrkgsllhl
tlpkkvpmltwpsllveadeqlcipplnsqtcllgseenlaplagekavppgndpvspamvrsrnpgkddcakeemavaa
daatlvdepesmvnlafvkndsyekgpdsvvvhvyvkeicrdtsrvlfreqdftlifqtrdgnflrlhpgcgphttfrwq
vklrnliepeqctfcftasridiclrkrqsqrwggleapaarvggakvavptgptpldstppggaphpltgqeearavek
dkskarsedtgldsvatrtpmehvtpkpethlaspkptcmvppmphspvsgdsveeeeeeekkvclpgftglvnlgntcf
mnsviqslsntrelrdffhdrsfeaeinynnplgtggrlaigfavllralwkgthhafqpsklkaivaskasqftgyaqh
daqefmaflldglhedlnriqnkpytetvdsdgrpdevvaeeawqrhkmrndsfivdlfqgqyksklvcpvcakvsitfd
pflylpvplpqkqkvlpvfyfarephskpikflvsvskenstasevldslsqsvhvkpenlrlaeviknrfhrvflpshs
ldtvspsdtllcfellsselakervvvlevqqrpqvpsvpiskcaacqrkqqsedeklkrctrcyrvgycnqlcqkthwp
dhkglcrpenigypflvsvpasrltyarlaqllegyarysvsvfqppfqpgrmalesqspgcttllstgsleagdserdp
iqppelqlvtpmaegdtglprvwaapdrgpvpstsgissemlasgpievgslpagervsrpeaavpgyqhpseamnahtp
qffiykidssnreqrledkgdtplelgddcslalvwrnnerlqefvlvaskelecaedpgsageaaraghftldqclnlf
trpevlapeeawycpqckqhreaskqlllwrlpnvlivqlkrfsfrsfiwrdkindlvefpvrnldlskfcigqkeeqlp
sydlyavinhyggmigghytacarlpndrssqrsdvgwrlfddstvttvdesqvvtryayvlfyrrrnspverppraghs
ehhpdlgpaaeaaasqasriwqeleaeeepvpegsgplgpwgpqdwvgplprgpttpdegclryfvlgtvaalvalvlnv
fyplvsqsrwr

110. Doa4p human (13) NP_003354
maegggcrerpdaetqkselgplmrttlqrgaqwylidsrwfkqwkkyvgfdswdmynvgehnlfpgpidnsglfsdp
esqtlkehlideldyvlvpteawnkllnwygcvegqqpivrkvvehglfvkhckvevyllelklcensdptnvlschfskad
tiatiekemrklfnipaeretrlwnkymsntyeqlskldntvqdaglyqgqvlviepqnedgtwprqtlqskssstapsrn
fttspkssaspyssvsasliangdststcgmhssgvsrggsgfsasyncqeppsshiqpglcglgnlgntcfmnsalqcl
sntapltdyflkdeyeaeinrdnplgmkgeiaeayaelikqmwsgrdahvapsmfktqvgrfapqfsgyqqqdsqellaf
lldglhedlnrvkkkpylelkdangrpdavvakeawenhrlrndsvivdtfhglfkstlvcpecakvsvtfdpfcyltlp
lplkkdrvmevflvpadphcrptqyrvtvplmgavsdlcealsrlsgiaaenmvvadvynhrfhkifqmdeglnhimprd
difvyevcstsvdgsecvtlpvyfrerksrpsstssasalygqplllsvpkhkltleslyqavcdrisryvkqplpdefg
ssplepgacngsrnscegedeeemehqeegkeqlsetegsgedepgndpsettqkkikgqpcpkrlftfslvnsygtadi
nslaadgklllklnsrstlamdwdretrrlyydeqeseayekhvsmlqpqkkkkttvalrdcielfttmetlgehdpwycp

nckkhqqatkkfdlwslpkilvvhlkrfsynrywrdkldtvvefpirglnmsefvcnlsarpyvydliavsnhygamgvg
hytayaknklngkwyyfddsnvslasedqivtkaayvlfyqrrddefykktpslsssgssdggtrpsssqqgfgddeacsm
dtn

111. Doa4p human (14) XP_003288
maegggcrerpdaetqkselgplmrttlqrgaqwylidsrwfkqwkkyvgfdswdmynvgehnlfpgpidnsglfsdp
esqtlkehlideldyvlvpteawnkllnwygcvegqqpivrkvvehglfvkhckvevyllelklcensdptnvlschfskad
tiatiekemrklfnipaeretrlwnkymsntyeqlskldntvqdaglyqgqvlviepqnedgtwprqtlqsksstapsrn
fttspkssaspyssvsasliangdststcgmhssgvsrggsgfsasyncqeppsshiqpglcglgnlgntcfmnsalqcl
sntapltdyflkdeyeaeinrdnplgmkgeiaeayaelikqmwsgrdahvaprmfktqvgrfapqfsgyqqqdsqellaf
lldglhedlnrvkkkpylelkdangrpdavvakeawenhrlrndsvivdtfhglfkstlvcpecakvsvtfdpfcyltlp
lplkkdrvmevflvpadphcrptqyrvtvplmgavsdlcealsrlsgiaaenmvvadvynhrfhkifqmdeglnhimprd
difvyevcstsvdgsecvtlpvyfrerksrpsstssasalygqplllsvpkhkltleslyqavcdrisryvkqplpdefg
ssplepgacngsrnscegedeeemehqeegkeqlsetegsgedepgndpsettqkkikgqpcpkrlftfslvnsygtadi
nslaadgkllklnsrstlamdwdsetrrlyydeqeseayekhvsmlqpqkkkkttvalrdcielfttmetlgehdpwycp
nckkhqqatkkfdlwslpkilvvhlkrfsynrywrdkldtvvefpirglnmsefvcnlsarpyvydliavsnhygamgvg
hytayaknklngkwyyfddsnvslasedqivtkaayvlfyqrrddefykktpslsssgssdggtrpsssqqgfgddeacsm
dtn

<u>Elp2p (5 sequences)</u>

112. Elp2p human (01) NP_060725
mvapvletshvfccpnrvrgvlnwssgprgllafgtscsvvlydplkrvvvtnlnghtarvnciqwickqdgspstelvs
ggsdnqvihweiednqllkavhlqghegpvyavhavyqrrtsdpalctlivsaaadsavrlwskkgpevmclqtlnfgng
falalclsflpntdvpilacgnddcrihifaqqndqfqkvlslcghedwirgvewaafgrdlflascsqdcliriwklyi
kstsletqdddnirlkentftienesvkiafavtletvlaghenwvnavhwqpvfykdgvlqqpvrllsasmdktmilwa
pdeesgvwleqvrvgevggntlgfydcqfnedgsmiiahafhgalhlwkqntvnprewtpeivisghfdgvqdlvwdpe
gefiitvgtdqttrlfapwkrkdqsqvtwheiarpqihgydlkclaminrfqfvsgadekvlrvfsaprnfvenfcaitgq
slnhvlcnqdsdlpegatvpalglsnkavfqgdiasqpsdeeelltstgfeyqqvafqpsiltepptedhllqntlwpev
qklyghgyeifcvtcnssktllasackaakkehaaiilwnttswkqvqnlvfhsltvtqmafspnekfllavsrdrtwsl
wkkqdtispefepvfslfaftnkitsvhsriiwscdwspdskyfftgsrdkkvvvwgecdstddciehnigpcssvldvg
gavtavsvcpvlhpsqryvvavglecgkiclytwkktdqvpeindwthcvetsqsqshtlairklcwkncsgkteqkeae
gaewlhfascgedhtvkihrvnkcal

113. Elp2p human (02) BAA91874
mvapvletshvfccpnrvrgvlnwssgprgllafgtscsvvlydplkrvvvtnlnghtarvnciqwickqdgspstelvs
ggsdnqvihweiednqllkavhlqghegpvyavhavyqrrtsdpalctlivsaaadsavrlwskkgpevmclqtlnfgng
falalclsflpntdvpilacgnddcrihifaqqndqfqkvlslcghedwirgvewaafgrdlflascsqdcliriwklyi
kstsletqdddnirlkentftienesvkiafavtletvlaghenwvnavhwqpvfykdgvlqqpvrllsasmdktmilwa
pdeesgvwleqvrvgevggntlgfydcqfnedgsmiiahafhgalhlwkqntvnprewtpeivisghfdgvqdlvwdpe
gefiitvgtdqttrlfapwkrkdqsqvtwheiarpqihgydlkclaminrfqfvsgadekvlrvfsaprnfvenfcaitgq
slnhvlcnqdsdlpegatvpalglsnkavfqgdiasqpsdeeelltstgfeyqqvafqpsiltepptedhllqntlwpev
qklyghgyeifcvtcnssktllasackaakkehaaiilwnttswkqvqnlvfhsltvtqmafspnekfllavsrdrtwsl
wkkqdtispefepvfslfaftnkitsvhsriiwscdwspdskyfftgsrdkkvvvwgecdstddciehnigpcssvldvg
gavtavsvcpvlhpsqryvvavglecgkiclytwkktdqvpeindwthcvetsqsqshtlairklcwkncsgkteqkeae
gaewlhfascgedhtvkihrvnkcal

114. Elp2p human (03) BAB14193
mvapvletshvfccpnrvrgvlnwssgprgllafgtscsvvlydplkrvvvtnlnghtarvnciqwickqdgspstelvs
ggsdnqvihweiednqllkavhlqghegpvyavhavyqrrtsdpalctlivsaaadsavrlwskkgpevpilacgnddcr
ihifaqqndqfqkvlslcghedwirgvewaafgrdlflascsqdcliriwklyikstsletqdddnirlkentftienes
vkiafavtletvlaghenwvnavhwqpvfykdgvlqqpvrllsasmdktmilwapdeesgvwleqvrvgevggntlgfy
dcqfnedgsmiiahafhgalhlwkqntvnpgewtpeivisghfdgvqdlvwdpegefiitvgtdqttrlfapwkrkdqsq
vtwheiarpqihgydlkclaminrfqfvsgadekvlrvfsaprnfvenfcaitgqslnhvlcnqdsdlpegatvpalglsn
kavfqgdiasqpsdeeelltstgfeyqqvafqpsiltepptedhllqntlwpevqklyghgyeifcvtcnssktllasac
kaakkehaaiilwnttswkqvqnlvfhsltvtqmafspnekfllavsrdrtwslwkkqdtispefepvfslfaftnkits
vhsriiwscdwspdskyfftgsrdkkvvvwgvcdstddciehnigpcssvldvggavtavsvcpvlhpsqryvvavglec
gkiclytwkktdqvpeindwthcvetsqsqshtlairklcwkncsgkteqkeaegaewlhfascgedhtvkihrvnkcal

115. Elp2p human (04) AF332505_1
mvapvletshvfccpnrvrgvlnwssgprgllafgtscsvvlydplkrvvvtnlnghtarvnciqwickqdgspstelvs
ggsdnqvihweiednqllkavhlqghegpvyavhavyqrrtsdpalctlivsaaadsavrlwskkgpevpilacgnddcr
ihifaqqndqfqkvlslcghedwirgvewaafgrdlflascsqdcliriwklyikstsletqdddnirlkentftienes
vkiafavtletvlaghenwvnavhwqpvfykdgvlqqpvrllsasmdktmilwapdeesgvwleqrewtpeivisghfd
gvqdlvwdpegefiitvgtdqttrlfapwkrkdqsqvtwheiarpqihgydlkclaminrfqfvsgadekvlrvfsaprnf
venfcaitgqslnhvlcnqdsdlpegatvpalglsnkavfqgdiasqpsdeeelltstgfeyqqvafqpsiltepptedh
llqntlwpevqklyghgyeifcvtcnssktllasackaakkehaaiilwnttswkqvqnlvfhsltvtqmafspnekfll
avsrdrtwslwkkqdtispefepvfslfaftnkitsvhsriiwscdwspdskyfftgsrdkkvvvwgvcdstddciehni
gpcssvldvggavtavsvcpvlhpsqryvvavglecgkiclytwkktdqvpeindwthcvetsqsqshtlairklcwknc
sgkteqkeaegaewlhfascgedhtvkihrvnkcal

116. Elp2p human (05) AAH09211
gtrllqntlwpevqklyghgyeifcvtcnssktllasackaakkehaaiilwnttswkqvqnlvfhsltvtqmafspnek
fllavsrdrtwslwkkqdtispefepvfslfaftnkitsvhsriiwscdwspdskyfftgsrdkkvvvwgecdstddcie
hnigpcssvldvggavtavsvcpvlhpsqryvvavglecgkiclytwkktdqvpeindwthcvetsqsqshtlairklcw
kncsgkteqkeaegaewlhfascgedhtvkihrvnkcal

Elp3p (5 sequences)

117. Elp3p human (01) AAH01240
mrqkrkgdlspaelmmltigdvikqlieaheqgkdidlnkvktktaakyglsaqprlvdiiaavppqyrkvlmpklkakp
irtasgiavvavmckphrcphisftgnicvycpggpdsdfeystqsytgyeptsmrairarydpflqtrhrieqlkqlgh
svdkvefivmggtfmalpeeyrdyfirnlhdalsghtsnniyeavkysersltkcigitietrpdycmkrhlsdmltygc
trleigvqsvyedvardtnrghtvkavcesfhlakdsgfkvvahmmpdlpnvglerdieqfteffenpafrpdglklypt
lvirgtglyelwksgryksyspsdlvelvarilalvppwtrvyrvqrdipmplvssgvehgnlrelalarmkdlgiqcrd
vrtrevgiqeihhkvrpyqvelvrrdyvanggwetflsyedpdqdiligllrlrkcseetfrfelgggvsivrelhvygs
vvpvssrdptkfqhqgfgmllmeeaeriareehgsgkiavisgvgtrnyyrkigyrlqgpymvkmlk

118. Elp3p human (02) BAB14138
mrqkrkgdlspaelmmltigdvikqlieaheqgkdidlnkvktktaakyglsaqprlvdiiaavppqyrkvlmpklkakp
irtasgiavvavmckphrcphisftgnicvycpggpdsdfeystqsytgyeptsmrairarydpflqtrhrieqlkqlgh

svdkvefivmggtfmalpeeyrdyfirnlhdalsghtsnniyeavkysersltkcigitietrpdycmkrhlsdmltygc
trleigvqsvyedvardtnrghtvmavcesfhlakdsgfkvvahmmpdlpnvglerdieqfteffenpafrpdglklypt
lvirgtglyelwksgryksyspsdlvelvarilalvppwtrvyrvqrdipmplvssgvehgnlrelalarmkdlgiqcrd
vrtrevgiqeihhkvrpyqvelvrrdyvanggwetflsyedpdqdiligllrlrkcseetfrfelgggvsivrelhvygs
vvpvssrdptkfqhqgfgmllmeeaeriareehgsgkiavisgvgtrnyyrkigyrlqgpymvkmlk

119. Elp3p human (03) NP_060561
mrqkrkgdlgpaelmmltigdvikqlieaheqgkdidlnkvktktaakyglsaqprlvdiiaavppqyrkvlmpklkakp
irtasgiavvavmckphrcphisftgnicvycpggpdsdfeystqsytgyeptsmrairarydpflqtrhrieqlkqlgh
svdkvefivmggtfmalpeeyrdyfirnlhdalsghtsnniyeavkysersltkcigitietrpdycmkrhlsdmltygc
trleigvqsvyedvardtnrghtvkavcesfhlakdsgfkvvahmmpdlpnvglerdieqfteffenpafrpdglklypt
lvirgtglyelwksgryksyspsdlvelvarilalvppwtrvyrvqrdipmplvssgvehgnlrelalarmkdlgiqcrd
vrtrevgiqeihhkvrpyqvelvrrdyvanggwetflsyedpdqdiligllrlrkcseriareehgsgkiavisgvgtrn
yyrkigyrlqgpymvkmlk

120. Elp3p human (04) BAA91600
mrqkrkgdlgpaelmmltigdvikqlieaheqgkdidlnkvktktaakyglsaqprlvdiiaavppqyrkvlmpklkakp
irtasgiavvavmckphrcphisftgnicvycpggpdsdfeystqsytgyeptsmrairarydpflqtrhrieqlkqlgh
svdkvefivmggtfmalpeeyrdyfirnlhdalsghtsnniyeavkysersltkcigitietrpdycmkrhlsdmltygc
trleigvqsvyedvardtnrghtvkavcesfhlakdsgfkvvahmmpdlpnvglerdieqfteffenpafrpdglklypt
lvirgtglyelwksgryksyspsdlvelvarilalvppwtrvyrvqrdipmplvssgvehgnlrelalarmkdlgiqcrd
vrtrevgiqeihhkvrpyqvelvrrdyvanggwetflsyedpdqdiligllrlrkcseriareehgsgkiavisgvgtrn
yyrkigyrlqgpymvkmlk

121. Elp3p human (05) XP_027454
mrqkrkgdlspaelmmltigdvikqlieaheqgkdidlnkvktktaakyglsaqprlvdiiaavppqyrkvlmpklkakp
irtasgiavvavmckphrcphisftgnicvycpggpdsdfeystqsytgyeptsmrairarydpflqtrhrieqlkqlgh
svdkvefivmggtfmalpeeyrdyfirnlhdalsghtsnniyeavkysersltkcigitietrpdycmkrhlsdmltygc
trleigvqsvyedvardtnrghtvkavcesfhlakdsgfkvvahmmpdlpnvglerdieqftgvf

Elp4p (4 sequences)

122. Elp4 human (01) NP_061913
maavatcgsvaastgsavatasksnvtsfqrrgprasvtndsgprlvsiagtrpsvrngqllvstglpaldqllgggglav
gtvllieedkyniyspllfkyflaegivnghtllvasakedpanilqelpaplldkckkefdedvynhktpesnikmki
awryqllpkmeigpvsssrfghyydaskrmpqelieasnwhgfflpekisstlkvepcsltpgytkllqfiqniiyeegf
dgsnpqkkqrnilrigiqnlgsplwgddiccaenggnshsltkflyvlrgllrtslsaciitmpthliqnkaiiarvttl
sdvvvglesfigseretnplykdyhglihirqiprlnnlicdesdvkdlafklkrklftierlhlppdlsdtvsrsskmd
laesakrlgpgcgmmaggkkhldf

123. Elp4 human (02) BAA91212
maavatcgsvaastgsavatasksnvtsfqrrgprasvtndsgprlvsiagtrpsvrngqllvstglpaldqllgggglav
gtvllieedkyniyspllfkyflaegivnghtllvasakedpanilqelpaplldkckkefdedvynhktpesnikmki
awryqllpkmeigpvsssrfghyydaskrmpqelieasnwhgfflpekisstlkvepcsltpgytkllqfiqniiyeegf
dgsnpqkkqrnilrigiqnlgsplwgddiccaenggnshsltkflyvlrgllrtslsaciitmpthliqnkaiiarvttl
sdvvvglesfigseretnplykdyhglihirqiprlnnlicdesdvkdlafklkrklftierlhlppdlsdtvsrsskmd

laesakrlgpgcgmmaggkkhldf

124. Elp4 human (03) CAB66612
maavatcgsvaastgsavatasksnvtsfqrrgprasvtndsgprlvsiagtrpsvrngqllvstglpaldqllggglav
gtvllieedkyniyspllfkyflaegivnghtllvasakedpanilqelpaplldkckkefdedvynhktpesnikmki
awryqllpkmeigpvsssrfghyydaskrmpqelieasnwhgfflpekisstlkvepcsltpgytkllqfiqniiyeegf
dgsnpqkkqrnilrigiqnlgsplwgddiccaenggnshsltkflyvlrgllrtslsaciitmpthliqnkaiiarvttl
sdvvvglesfigseretnplykdyhglihirqiprlnnlicdesdvkdlafklkrklftierlhlppdlsdtvsrsskmd
laesakrlgpgcgmmaggkkhldf

125. Elp4 human (04) AAH12514
maavatcgsvaastgsavatasksnvtsfqrrgprasvtndsgprlvsiagtrpsvrngqllvstglpaldqllggglav
gtvllieedkyniyspllfkyflaegivnghtllvasakedpanilqelpaplldkckkefdedvynhktpesnikmki
awryqllpkmeigpvsssrfghyydaskrmpqelieasnwhgfflpekisstlkvepcsltpgytkllqfiqniiyeegf
dgsnpqkkqrnilrigiqnlgsplwgddiccaenggnshsltkflyvlrgllrtslsaciitmpthliqnkaiiarvttl
sdvvvglesfigseretnplykdyhglihirqiprlnnlicdesdvkdlafklkrklftieagvqwhdlgsrrprllgsg
gspasaslvagitgahhhaqlifvflvemgfhhvgqaglelltsgdssasasqsagiagmsyrarpralyfkenkskvga
rqlletreehlssrllilltqaerlcmgrrfftafhifnelpckgdciclqtcqtq

Erv14p (1 sequences)

126. Erv14p human (01) NP_054903
meavvfvfsllldccaliflsvyfiitlsdlecdyinarsccsklnkwvipelightivtvlllmslhwfifllnlpvatw
niyryimvpsgnmgvfdpteihnrgqlkshmkeamiklgfhllcffmylysmilalind

Iki3p (5 sequences)

127. Iki3p human (01) XP_047455
mrnlklfrtlefrdiqgpgnpqcfslrteqgtvligsehglievdpvsrevknevslvaegflpedgsgrivgvqdlldq
esvcvatasgdvilcslstqqlecvgsvasgisvmswspdqelvllatgqqtlimmtkdfepileqqihqddfgeskfit
vgwgrketqfhgsegrqaafqmqmhesalpwddhrpqvtwrgdgqffavsvvcpetgarkvrvwnrefalqstsepva
glgpalawkpsgsliastqdkpnqqdivffekngllhghftlpflkdevkvndllwnadssvlavwledlqreessipktcv
qlwtvgnyhwylkqslsfstcgkskivslmwdpvtpyrlhvlcqgwhylaydwhwttdrsvgdnssdlsnvavidgnrv
lvtvfrqtvvpppmctyqllfphpvnqvtflahpqksndlavldasnqisvykcgdcpsadptvklgavggsgfkvclrtp
hlekrykiqfennedqdvnplklglltwieedvflavshsefsprsvihhltaassemdeehgqlnvsssaavdgviisl
ccnsktksvvlqladgqifkylwespslaikpwknsggfpvrfpypctqtelamigeeecvlgltdrcrffindievasn
itsfavydeflllltthshtcqcfclrdasfktlqaglssnhvshgevlrkvergsrivtvvpqdtklvlqmprgnlevvh
hralvlaqirkwldklmfkeafecmrklrinlnliydhnpkvflgnvetfikqidsvnhinlfftelkeedvtktmypap
vtssvylsrdpdgnkidlvcdamravmesinphkyclsiltshvkkttpeleivlqkvhelqgnapsdpdavsaeealky
llhlvdvnelydhslgtydfdlvlmvaeksqkdpkeylpflntlkkmetnyqrftidkylkryekaighlskcgpeyfpe
clnlikdknlynealklyspssqqyqdisiaygehlmqehmyepaglmfarcgahekalsafltcgnwkqalcvaaqlnf
tkdqlvglgrtlagklveqrkhidaamvleecaqdyeeavllllegaaweealrlvykynrldiietnvkpsileaqkny
mafldsqtatfsrhkkrllvvrelkeqaqqaglddevphgqesdlfsetssvvsgsemsgkyshsnsrisarssknrrka
erkkhslkegspledlallealsevvqntenlkdevyhilkvlflfefdeqgrelqkafedtlqlmerslpeiwtltyqq
nsatpvlgpnstansimasyqqqktsvpvldaelfippkinrrtqwklslld

128. Iki3p human (02) AF153419_1
mrnlklfrtlefrdiqgpgnpqcfslrteqgtvligsehglievdpvsrevknevslyaegflpedgsgrivgvqdlldq
esvcvatasgdvilcslstqqlecvgsvasgisvmswspdqelvllatgqqtlimmtkdfepileqqihqddfgeskfit
vgwgrketqfhgsegrqaafqmqmhesalpwddhrpqvtwrgdgqffavsvvcpetgarkvrvwnrefalqstsepva
glgpalawkpsgsliastqdkpnqqdivffekngllhghftlpflkdevkvndllwnadssvlavwledlqreessipktcv
qlwtvgnyhwylkqslsfstcgkskivslmwdpvtpyrlhvlcqgwhylaydwhwttdrsvgdnssdlsnvavidgnrv
lvtvfrqtvvpppmctyqllfphpvnqvtflahpqksndlavldasnqisvykcgdcpsadptvklgavggsgfkvclrtp
hlekrykiqfennedqdvnplklglltwieedvflavshsefsprsvihhltaassemdeehgqlnvsssaavdgviisl
ccnsktksvvlqladgqifkylwespslaikpwknsggfpvrfpypctqtelamigeeecvlgltdrcrffindievasn
itsfavydeflllttshshtcqcfclrdasfktlqaglssnhvshgevlrkvergsrivtvvpqdtklvlqmprgnlevvh
hralvlaqirkwldklmfkeafecmrklrinlnliydhnpkvflgnvetfikqidsvnhinlfftelkeedvtktmypap
vtssvylsrdpdgnkidlvcdamravmesinphkyclsiltshvkkttpeleivlqkvhelqgnapsdpdavsaeealky
llhlvdvnelydhslgtydfdlvlmvaeksqkdpkeylpflntlkkmetnyqrftidkylkryekaighlskcgpeyfpe
clnlikdknlynealklyspssqqyqdisiaygehlmqehmyepaglmfarcgahekalsafltcgnwkqalcvaaqlnf
tkdqlvglgrtlagklveqrkhidaamvleesaqdyeeavllllegaaweealrlvykynrldiietnvkpsileaqkny
mafldsqtatfsrhkkrllvvrelkeqaqqaglddevphgqesdlfsetssvvsgsemsgkyshsnsrisarssknrrka
erkkhslkegspledlallealsevvqntenlkdevyhilkvlflfefdeqgrelqkafedtlqlmerslpeiwtltyqq
nsatpvlgpnstansimasyqqqktsvpvldaelfippkinrrtqwklslld

129. Iki3p human (03) IKAP_HUMAN
mrnlklfrtlefrdiqgpgnpqcfslrteqgtvligsehglievdpvsrevknevslyaegflpedgsgrivgvqdlldq
esvcvatasgdvilcslstqqlecvgsvasgisvmswspdqelvllatgqqtlimmtkdfepileqqihqddfgeskfit
vgwgrketqfhgsegrqaafqmqmhesalpwddhrpqvtwrgdgqffavsvvcpetgarkvrvwnrefalqstsepva
glgpalawkpsgsliastqdkpnqqdivffekngllhghftlpflkdevkvndllwnadssvlavrledlqrekssipktcv
qlwtvgnyhwylkqslsfstcgkskivslmwdpvtpyrlhvlcqgwhylaydwhwttdrsvgdnssdlsnvavidgnrv
lvtvfrqtvvpppmctyqllfphpvnqvtflahpqksndlavldasnqisvykcgdcpsadptvklgavggsgfkvclrtp
hlekrykiqfennedqdvnplklglltwieedvflavshsefsprsvihhltaassemdeehgqlnvsssaavdgviisl
ccnsktksvvlqladgqifkylwespslaikpwknsggfpvrfpypctqtelamigeeecvlgltdrcrffindievasn
itsfavydeflllttshshtcqcfclrdasfktlqaglssnhvshgevlrkvergsrivtvvpqdtklvlqmprgnlevvh
hralvlaqirkwldklmfkeafecmrklrinlnpiydhnpkvflgnvetfikqidsvnhinlfftelkeedvtktmypap
vtssvylsrdpdgnkidlvcdamravmesinphkyclsiltshvkkttpeleivlqkvhelqgnapsdpdavsaeealky
llhlvdvnelydhslgtydfdlvlmvaeksqkdpkeylpflntlkkmetnyqrftidkylkryekaighlskcgpeyfpe
clnlikdknlynealklyspssqqyqdisiaygehlmqehmyepaglmfarcgahekalsafltcgnwkqalcvaaqlnf
tkdqlvglgrtlagklveqrkhidaamvleesaqdyeeavllllegaaweealrlvykynrldiietnvkpsileaqkny
mafldsqtatfsrhkkrllvvrelkeqaqqaglddevphgqesdlfsetssvvsgsemsgkyshsnsrisarssknrrka
erkkhslkegspledlallealsevvqntenlkdevyhilkvlflfefdeqgrelqkafedtlqlmerslpeiwtltyqq
nsatpvlgpnstansimasyqqqktsvpvldaelfippkinrrtqwklslld.

130. Iki3p human (04) NP_003631
mrnlklfrtlefrdiqgpgnpqcfslrteqgtvligsehglievdpvsrevknevslvaegflpedgsgrivgvqdlldq
esvcvatasgdvilcslstqqlecvgsvasgisvmswspdqelvllatgqqtlimmtkdfepileqqihqddfgeskfit
vgwgrketqfhgsegrqaafqmqmhesalpwddhrpqvtwrgdgqffavsvvcpetgarkvrvwnrefalqstsepva
glgpalawkpsgsliastqdkpnqqdivffekngllhghftlpflkdevkvndllwnadssvlavrledlqrekssipktcv
qlwtvgnyhwylkqslsfstcgkskivslmwdpvtpyrlhvlcqgwhylaydwhwttdrsvgdnssdlsnvavidgnrv
lvtvfrqtvvpppmctyqllfphpvnqvtflahpqksndlavldasnqisvykcgdcpsadptvklgavggsgfkvclrtp
hlekrykiqfennedqdvnplklglltwieedvflavshsefsprsvihhltaassemdeehgqlnvsssaavdgviisl

ccnsktksvvlqladgqifkylwespslaikpwknsggfpvrfpypctqtelamigeeecvlgltdrcrffindievasn
itsfavydefllltthshtcqcfclrdasfktlqaglssnhvshgevlrkvergsrivtvvpqdtklvlqmprgnlevvh
hralvlaqirkwldklmfkeafecmrklrinlnpiydhnpkvflgnvetfikqidsvnhinlfftelkeedvtktmypap
vtssvylsrdpdgnkidlvcdamravmesinphkyclsiltshvkkttpeleivlqkvhelqgnapsdpdavsaeealky
llhlvdvnelydhslgtydfdlvlmvaeksqkdpkeylpflntlkkmetnyqrftidkylkryekaighlskcgpeyfpe
clnlikdknlynealklyspssqqyqdisiaygehlmqehmyepaglmfarcgahekalsafltcgnwkqalcvaaqlnf
tkdqlvglgrtlagklveqrkhidaamvleecaqdyeeavlllegaaweealrlvykynrldiietnvkpsileaqkny
mafldsqtatfsrhkkrllvvrelkeqaqqaglddevphgqesdlfsetssvvsgsemsgkyshsnsrisarssknrrka
erkkhslkegspledlallealsevvqntenlkdevyhilkvlflfefdeqgrelqkafedtlqlmerslpeiwtltyqq
nsatpvlgpnstansimasyqqqktsvpvldaelfippkinrrtqwklslld

131. Iki3p human (05) AAC64258
mrnlklfrtlefrdiqgpgnpqcfslrteqgtvligsehglievdpvsrevknevslvaegflpedgsgrivgvqdlldq
esvcvatasgdvilcslstqqlecvgsvasgisvmswspdqelvllatgqqtlimmtkdfepileqqihqddfgeskfit
vgwgrketqfhgsegrqaafqmqmhesalpwddhrpqvtwrgdgqffavsvvcpetgarkvrvwnrefalqstsepva
glgpalawkpsgsliastqdkpnqqdivffekngllhghftlpflkdevkvndllwnadssvlavrledlqrekssipktcv
qlwtvgnyhwylkqslsfstcgkskivslmwdpvtpyrlhvlcqgwhylaydwhwttdrsvgdnssdlsnvavidgnrv
lvtvfrqtvvpppmctyqllfphpvnqvtflahpqksndlavldasnqisvykcgdcpsadptvklgavggsgfkvclrtp
hlekrykiqfennedqdvnplklglltwieedvflavshsefspsrsvihhltaassemdeehgqlnvsssaavdgviisl
ccnsktksvvlqladgqifkylwespslaikpwknsggfpvrfpypctqtelamigeeecvlgltdrcrffindievasn
itsfavydefllltthshtcqcfclrdasfktlqaglssnhvshgevlrkvergsrivtvvpqdtklvlqmprgnlevvh
hralvlaqirkwldklmfkeafecmrklrinlnpiydhnpkvflgnvetfikqidsvnhinlfftelkeedvtktmypap
vtssvylsrdpdgnkidlvcdamravmesinphkyclsiltshvkkttpeleivlqkvhelqgnapsdpdavsaeealky
llhlvdvnelydhslgtydfdlvlmvaeksqkdpkeylpflntlkkmetnyqrftidkylkryekaighlskcgpeyfpe
clnlikdknlynealklyspssqqyqdisiaygehlmqehmyepaglmfarcgahekalsafltcgnwkqalcvaaqlnf
tkdqlvglgrtlagklveqrkhidaamvleecaqdyeeavlllegaaweealrlvykynrldiietnvkpsileaqkny
mafldsqtatfsrhkkrllvvrelkeqaqqaglddevphgqesdlfsetssvvsgsemsgkyshsnsrisarssknrrka
erkkhslkegspledlallealsevvqntenlkdevyhilkvlflfefdeqgrelqkafedtlqlmerslpeiwtltyqq
nsatpvlgpnstansimasyqqqktsvpvldaelfippkinrrtqwklslld

Kcs1p (4 sequences)

132. Kcs1p human (01) XP_084209
mvvqnsadagdmragvqlepflhqvgghmsvmkydehtvckplvsreqrfyeslplamkrftpqykgtvtvhlwkdst
ghlslvanpvkesqepfkvstesaavaiwqtlqqttgsngsdctlaqwphaqlarspkespakallrsephlntpafslved
tngnqverksfnpwglqchqahltrlcseypenkrhrflllenvvsqythpcvldlkmgtrqhgddaseekkarhmrkca
qstsaclgvricgmqvyqtdkkyflckdkyygrklsvegfrqalyqflhngshlrrellepilhqlrallsvirsqssyr
fyssslIviydgqepperapgsphpheapqaahgsspggltkvdirmidfahttykgywnehttydgpdpgyifglenli
rilqdiqege

133. Kcs1p human (02) AF3938
mvvqnsadagdmragvqlepflhqvgghmsvmkydehtvckplvsreqrfyeslpqamkrftpqykgtvtvhlwkds
tghlslvanpvkesqepfkvstesaavaiwqtlqqttgsngsdctlaqwphaqlarspkespakallrsephlntpafslved
tngnqverksfnpwglqchqahltrlcseypenkrhrflllenvvsqythpcvldlkmgtrqhgddaseekkarhmrkca
qstsaclgvricgmqvyqtdkkyflckdkyygrklsvegfrqalyqflhngshlrrellepilhqlrallsvirsqssyr
fyssslIviydgqepperapgsphpheapqaahgsspggltkvdirmidfahttykgywnehttydgpdpgyifglenli

rilqdiqege

134. Kcs1p human (03) NP_473452
maatdpcqwphaqlarspkespakallrsephlntpafslvedtngnqverksfnpwglqchqahltrlcseypenkrhr
flllenvvsqythpcvldlkmgtrqhgddaseekkarhmrkcaqstsaclgvricgmqvyqtdkkyflckdkyygrklsv
egfrqalyqflhngshlrrellepillqlrallsiirsqssyrfysssllviydgqepperapgsphpheapqaahgssp
ggltkvdirmidfahttykgywnehttydgpdpgyifglenlirilqdiqege

135. Kcs1p human (04) XP_028610
mldgnsglssekishnpwslrchkqqlsrmrseskdrklykflllenvvhhfkypcvldlkmgtrqhgddasaekaarqm
rkceqstsatlgvrvcgmqvyqldtghylcrnkyygrglsiegfrnalyqylhngldlrrdlfepilsklrglkavlerq
asyrfysssllviydgkecraescldrrsemrlkhldmvlpevasscgpstspsntspeagpssqpkvdvrmidfahstf
kgfrddptvhdgpdrgyvfglenlisimeqmrdenq

Kti12p (4 sequences)

136. Kti12p human (01) XP_053554
mplvvfcglpysgksrraeelrvalaaegravyvvddaavlgaedpavygdsarekalrgalrasverrlsrhdvvilds
lnyikgfryelyclaraartplclvycvrpggpiagpqvaganenpgrnvsvswrpraeedgraqaagssvlrelhtads
vvngsaqadvpkelereesgaaespalvtpdseksakhgsgafyspellealtlrfeapdsrnrwdrplftlvgleeplp
lagirsalfenrappphqstqsqplasgsflhqldqvtsqvlaglmeaqksavpgdlltlpgttehlrftrpltmaelsr
lrrqfisytkmhpnnenlpqlanmflqylsqslh

137. Kti12p human (02) NP_612426
mplvvfcglpysgksrraeelrvalaaegravyvvddaavlgaedpavygdsarekalrgalrasverrlsrhdvvilds
lnyikgfryelyclaraartplclvycvrpggpiagpqvaganenpgrnvsvswrpraeedgraqaagssvlrelhtads
vvngsaqadvpkelereesgaaespalvtpdseksakhgsgafyspellealtlrfeapdsrnrwdrplftlvgleeplp
lagirsalfenrappphqstqsqplasgsflhqldqvtsqvlaglmeaqksavpgdlltlpgttehlrftrpltmaelsr
lrrqfisytkmhpnnenlpqlanmflqylsqslh

138. Kti12p human (03) AAH12173
mplvvfcglpysgksrraeelrvalaaegravyvvddaavlgaedpavygdsarekalrgalrasverrlsrhdvvilds
lnyikgfryelyclaraartplclvycvrpggpiagpqvaganenpgrnvsvswrpraeedgraqaagssvlrelhtads
vvngsaqadvpkelereesgaaespalvtpdseksakhgsgafyspellealtlrfeapdsrnrwdrplftlvgleeplp
lagirsalfenrappphqstqsqplasgsflhqldqvtsqvlaglmeaqksavpgdlltlpgttehlrftrpltmaelsr
lrrqfisytkmhpnnenlpqlanmflqylsqslh

139. Kti12p human (04) AF327348_1
mplvvfcglpysgksrraeelrvalaaegravyvvddaavlgaedpavygdsarekalrgalrasverrlsrhdvvilds
lnyikgfryelyclaraartplclvycvrpggpiagpqvaganenpgrnvsvswrpraeedgraqaagssvlrelhtads
vvngsaqadvpkelereesgaaespalvtpdseksakhgsgafyspellealtlrfeapdsrnrwdrplftlvgleeplp
lagirsalfenrappphqstqsqplasgsflhqldqvtsqvlaglmeaqksavpgdlltlpgttehlrftrpltmaelsr
lrrqfisytkmhpnnenlpqlanmflqylsqslh

Lsm1p (9 sequences)

140. Lsm1p human (01) NP_055277
mnympgtasliedidkkhlvllrdgrtligflrsidqfanlvlhqtverihvgkkygdiprgifvvrgenvvllgeidle
kesdtplqqvsieeileeqrveqqtkleaeklkvqalkdrglsipradtldey

141. Lsm1p human (02) AAB62189
mnympgtasliedidkkhlvllrdgrtligflrsidqfanlvlhqtverihvgkkygdiprgifvvrgenvvllgeidle
kesdtplqqvsieeileeqrveqqtkleaeklkvqalkdrglsipradtldey

142. Lsm1p human (03) CAB45865
mnympgtasliedidkkhlvllrdgrtligflrsidqfanlvlhqtverihvgkkygdiprgifvvrgenvvllgeidle
kesdtplqqvsieeileeqrveqqtkleaeklkvqalkdrglsipradtldey

143. Lsm1p human (04) AAH01767
mnympgtasliedidkkhlvllrdgrtligflrsidqfanlvlhqtverihvgkkygdiprgifvvrgenvvllgeidle
kesdtplqqvsieeileeqrveqqtkleaeklkvqalkdrglsipradtldey

144. Lsm1p human (05) NP_057284
mtsalenyinrtvavitsdgrmivgtlkgfdqtinlildeshervfsssqgveqvvlglyivrgdnvavigeideetdsa
ldlgniraeplnsvah

145. Lsm1p human (06) AAD15542
mtsalenyinrtvavitsdgrmivgtlkgfdqtinlildeshervfsssqgveqvvlglyivrgdnvavigeideetdsa
ldlgniraeplnsvah

146. Lsm1p human (07) AAD56232
mtsalenyinrtvavitsdgrmivgtlkgfdqtinlildeshervfsssqgveqvvlglyivrgdnvavigeideetdsa
ldlgniraeplnsvah

147. Lsm1p human (08) AAH02742
mtsalenyinrtvavitsdgrmivgtlkgfdqtinlildeshervfsssqgveqvvlglyivrgdnvavigeideetdsa
ldlgniraeplnsvah

148. Lsm1p human (09) AAH22440
mtsalenyinrtvavitsdgrmivgtlkgfdqtinlildeshervfsssqgveqvvlglyivrgdnvavigeideetdsa
ldlgniraeplnsvah

<u>**Mad2p (6 sequences)**</u>

149. Mad2p human (01) NP_002349
malqlsreqgitlrgsaeivaeffsfginsilyqrgiypsetftrvqkygltllvttdlelikylnnvveqlkdwlykcs
vqklvvvisniesgevlerwqfdiecdktakddsapreksqkaiqdeirsvirqitatvtflpllevscsfdlliytdkd
lvvpekweesgpqfitnseevrlrsftttihkvnsmvaykipvnd

150. Mad2p human (02) 18655665
xsitlrgsaeivaeffsfginsilyqrgiypsetftrvqkygltllvttdlelikylnnvveqlkdwlykcsvqklvvvi
sniesgevlerwqfdiecdktakddsapreksqkaiqdeirsvirqitatvtflpllevscsfdlliytdkdlvvpekwe

esgpqfitnseevrlrsftttihkvnsmvaykipvnd

151. Mad2p human (03) 7245371
gsitlrgsaeivaeffsfginsilyqrgiypsetftrvqkygltllvttdlelikylnnvveqlkdwlykcsvqklvvvi
sniesgevlerwqfdiecdktakddsapreksqkaiqdeirsvirqitatvtflpllevscsfdlliytdkdlvvpekwe
esgpqfitnseevrlrsftttihkvns

152. Mad2p human (04) XP_058210
malqlsreqgitlrgsaeivdeffsfginsilyqrgiypseiftrvqkygltllvttdlelikylnnvveqlkdwlykcs
vqklvvvisniesgevler

153. Mad2p human (05) XP_091252
mldgqspllisvprqqlrtlpgshvylqlgeelcqpragagthldqdlpdapgppgervvtfcdqfgkrlggpatgqcgn
pgfefpprrcfrtesplnalpqgssifskfivfvkatqaasgaaisiwspcslamprsllwdfgalfpleapwllraepa
eknehstaataaanlypnraarknpdlldgvvkasgfseqfllltapleeiegqhtlflevvetleegfwlfknwkvtae
esvpvthsnvtaqaitrdtciqhkaaaqgkvnywmstwsskatnclgspflnvskgiqqrglfcpaavdsvwclfwacyq
hflitvtdealrtslvcaaawecltlaldgtpptgiiaaehrclwpprvsygshcgyceadpliisqvkhtkirvdsrls
lhqcafevctvyypgstrggflcgilssavgpvnivcqvkacilvhgpahalklswekditlcrsakivvkffsfginsi
lfqhgiypsgtftpvwkygltllvttnlelmkhlnntveqlkhwlykrsgqkligvisttesdevlqrwqfdpkcdktak
dhlgpre

154. Mad2p human (06) XP_085141
malqlsreqgitlrgsaeivdeffsfginsilyqrgiypseiftrvqkygltllvttdlelikylnnvveqlkvhpeksl
rklfrmksvqssdrsqlq

<u>**Mck1p (7 sequences)**</u>

155. Mck1p human (01) NP_063937
msgggpsgggpggsgrartssfaepggggggggggpggsasgpggtgggkasvgamgggvgasssgggpggsgggg
sggpgagtsfpppgvklgrdsgkvttvvatlgqgpersqevaytdikvigngsfgvvyqarlaetrelvaikkvlqdkrfknr
elqimrkldhcnivrlryffyssgekkdelylnlvleyvpetvyrvarhftkakltipilyvkvymyqlfrslayihsqgv
chrdikpqnllvdpdtavlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidvwsagcvlaelllgqpif
pgdsgvdqlveiikvlgtptreqiremnpnytefkfpqikahpwtkvfksrtppeaialcsslleytpssrlspleacah
sffdelrclgtqlpnnrplpplfnfsagelsiqpslnailipphlrspsgtttltpssqaltetptssdwqstdatptlt
nss

156. Mck1p human (02) P49840
msgggpsgggpggsgrartssfaepggggggggggpggsasgpggtgggkasvgamgggvgasssgggpggsgggg
sggpgagtsfpppgvklgrdsgkvttvvatlgqgpersqevaytdikvigngsfgvvyqarlaetrelvaikkvlqdkrfknr
elqimrkldhcnivrlryffyssgekkdelylnlvleyvpetvyrvarhftkakltipilyvkvymyqlfrslayihsqgv
chrdikpqnllvdpdtavlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidvwsagcvlaelllgqpif
pgdsgvdqlveiikvlgtptreqiremnpnytefkfpqikahpwtkvfksrtppeaialcsslleytpssrlspleacah
sffdelrclgtqlpnnrplpplfnfsagelsiqpslnailipphlrspagtttltpssqaltetptssdwqstdatptlt
nss

157. Mck1p human (03) AAH00251
msgrprttsfaesckpvqqpsafgsmkvsrdkdgskvttvvatpgqgpdrpqevsytdtkvigngsfgvvyqaklcdsge
lvaikkvlqdkrfknrelqimrkldhcnivrlryffyssgekkdevylnlvldyvpetvyrvarhysrakqtlpviyvkl
ymyqlfrslayihsfgichrdikpqnllldpdtavlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidv
wsagcvlaelllgqpifpgdsgvdqlveiikvlgtptreqiremnpnytefkfpqikahpwtkdssgtghftsgvrvfrp
rtppeaialcsrlleytptarltpleacahsffdelrdpnvklpngrdtpalfnfttqelssnpplatilippphariqaa
astptnataasdantgdrgqtnnaasasasnst

158. Mck1p human (04) 18158777
msgrprttsfaesckpvqqpsafgsmkvsrdkdgskvttvvatpgqgpdrpqevsytdtkvigngsfgvvyqaklcdsge
lvaikkvlqdkrfknrelqimrkldhcnivrlryffyssgekkdevylnlvldyvpetvyrvarhysrakqtlpviyvkl
ymyqlfrslayihsfgichrdikpqnllldpdtavlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidv
wsagcvlaelllgqpifpgdsgvdqlveiikvlgtptreqiremnpnytefkfpqikahpwtkvfrprtppeaialcsrl
leytptarltpleacahsffdelrdpnvklpngrdtpalfnfttqelssnpplatilippphariqaaastptnataasda
ntgdrgqtnnaasasasnst

159. Mck1p human (05) 18655516
skvttvvatpgqgpdrpqevsytdtkvigngsfgvvyqaklcdsgelvaikkvlqgkafknrelqimrkldhcnivrlry
ffyssgekkdevylnlvldyvpetvyrvarhysrakqtlpviyvklymyqlfrslayihsfgichrdikpqnllldpdta
vlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidvwsagcvlaelllgqpifpgdsgvdqlveiikvlg
tptreqiremnpnytefafpqikahpwtkvfrprtppeaialcsrlleytptarltpleacahsffdelrdpnvklpngr
dtpalfnfttqelssnpplatilippphari

160. Mck1p human (06) 18655515
skvttvvatpgqgpdrpqevsytdtkvigngsfgvvyqaklcdsgelvaikkvlqgkafknrelqimrkldhcnivrlry
ffyssgekkdevylnlvldyvpetvyrvarhysrakqtlpviyvklymyqlfrslayihsfgichrdikpqnllldpdta
vlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidvwsagcvlaelllgqpifpgdsgvdqlveiikvlg
tptreqiremnpnytefafpqikahpwtkvfrprtppeaialcsrlleytptarltpleacahsffdelrdpnvklpngr
dtpalfnfttqelssnpplatilippphariqa

161. Mck1p human (07) NP_002084
msgrprttsfaesckpvqqpsafgsmkvsrdkdgskvttvvatpgqgpdrpqevsytdtkvigngsfgvvyqaklcdsge
lvaikkvlqdkrfknrelqimrkldhcnivrlryffyssgekkdevylnlvldyvpetvyrvarhysrakqtlpviyvkl
ymyqlfrslayihsfgichrdikpqnllldpdtavlklcdfgsakqlvrgepnvsyicsryyrapelifgatdytssidv
wsagcvlaelllgqpifpgdsgvdqlveiikvlgtptreqiremnpnytefkfpqikahpwtkvfrprtppeaialcsrl
leytptarltpleacahsffdelrdpnvkhpngrdtpalfnfttqelssnpplatilippphariqaaastptnataasda
ntgdrgqtnnaasasasnst

<u>Nat1p (2 sequences)</u>

162. Nat1p human (01) NP_476516
mpavslppkenalfkrilrcyehkqyrnglkfckqilsnpkfaehgetlamkgltlnclgkkeeayelvrrglrndlksh
vcwhvygllqrsdkkydeaikcyrnalkwdkdnlqilrdlsllqiqmrdlegyretryqllqlrpaqraswigyaiayhl
ledyemaakileefrktqqtspdkvdyeysellllyqnqvlreaglyrealehlctyekqicdklaveetkgelllqlcrl
edaadvyrglqernpenwayykglekalkpanmlerlkiyeeawtkyprglvprrlplnflsgekfkecldkflrmnfsk
gcppvfntlrslykdkekvaiieelvvgyetslkscrlfnpnddgkeepptllwvqyylaqhydkigqpsialeyinta

Figure 4

iestptlielflvkakiykhagnikeaarwmdeaqaldtadrfinskcakymlkanlikeaeemcskftregtsavenln
emqcmwfqtecaqaykamnkfgealkkcheierhfieitddqfdfhtycmrkitlrsyvdllkledvlrqhpfyfkaari
aieiylklhdnpltdenkeheadtanmsdkelkklrnkqrraqkkaqieeekknaekekqqrnqkkkkddddeeiggpke
elipeklakvetpleeaikfltplknlvknkiethlfafeiyfrkekfllmlqsvkrafaidsshpwlhecmirlfntav
ceskdlsdtvrtvlkqemnrlfgatnpknfnetflkrnsdslphrlsaakmvyyldpssqkraielattldesltnrnlq
tcmevlealydgslgdckeaaeiyranchklfpyalafmppgyeedmkitvngdssaeaeelanei

163. Nat1p human (02) NP_079361
mpavslppkenalfkrilrcyehkqyrnglkfckqilsnpkfaehgetlamkgltlnclgkkeeayelvrrglrndlksh
vcwhvygllqrsdkkydeaikcyrnalkwdkdnlqilrdlsllqiqmrdlegyretryqllqlrpaqraswigyaiayhl
ledyemaakileefrktqqtspdkvdyeysellyqnqvlreaglyrealehlctyekqicdklaveetkgelllqlcrl
edaadvyrglqernpenwayykglekalkpanmlerlkiyeeawtkyprglvprrlplnflsgekfkecldkflrmnfsk
gcppvfntlrslykdkekvaiieelvvgyetslkscrlfnpnddgkeepptllwvqyylaqhydkigqpsialeyinta
iestptlielflvkakiykhagnikeaarwmdeaqaldtadrfinskcakymlkanlikeaeemcskftregtsavenln
emqcmwfqtecaqaykamnkfgealkkcheierkslmtsltfihtv

Nat3p (4 sequences)

164. Nat3p human (01) CAB66576
mttlraftcddlfrfnninldpltetygipfylqylahwpeyfivavapggelmgyimgkaegsvareewhghvtalsva
pefrrlglaaklmelleeiserkggffvdlfvrvsnqvavnmykqlgysvyrtvieyysasngepdedaydmrkalsrdt
ekksiiplphpvrpedie

165. Nat3p human (02) NP_057184
mttlraftcddlfrfnninldpltetygipfylqylahwpeyfivaeapggelmgyimgkaegsvareewhghvtalsva
pefrrlglaaklmelleeiserkggffvdlfvrvsnqvavnmykqlgysvyrtvieyysasngepdedaydmrkalsrdt
ekksiiplphpvrpedie

166. Nat3p human (03) CAC01670
nldpltetygipfylqylahwpeyfivaeapggelmgyimgkaegsvareewhghvtalsvapefrrlglaaklmellee
iserkggffvdlfvrvsnqvavnmykqlgysvyrtvieyysasngepdedaydmrkalsrdtekksiiplphpvrpedie

167. Nat3p mouse (04) AAH27219
mnirnarpedlmnmqhcnllclpenyqmkyyfyhglswpqlsyiaedengkivgyvlakmeedpddvphghitslav
krshrrlglaqklmdqasramienfnakyvslhvrksnraalhlysntlnfqisevepkyyadgedayamkrdltqmadep
asgpgssclls gdlgpvsfhplpsgllaaaeaapgaegkgqahgsgglgeqsgeqrqrafelrrgls

Nup84p (1 sequence)

168. Nup84p human (01) NP_065134
mdrsgfgeisspvireaevtrtarkqsaqkrvllqasqdenfgnttprnqviprtpssfrqpftptsrsllrqpdiscil
gtggksprltqssgffgnlsmvtnlddsnwaaafssqrsglftntephsitedvtisavmlreddpgeaasmsmfsdflq
sflkhsssstvfdlveeyenicgsqvnilskivsratpglqkfsktasmlwllqqemvtwrllaslyrdriqsaleeesvf
avtavnasektvvealfqrdslvrqsqlvvdwlesiakdeigefsdniefyaksvywentlhtlkqrqltsyvgsvrplv
teldpdapirqkmplddldredevrllkylftliragmteeaqrlckrcgqawraatlegwklyhdpnvnggtelepveg
npyrriwkiscwrmaedelfnryeraiyaalsgnlkqllpvcdtwedtvwayfrvmvdslveqeiqtsvatldeteelpr

eylganwtlekvfeelqatdkkrvleenqehyhivqkflilgdidglmdefskwlsksrnnlpghllrfmthlilffrtl
glqtkeevsievlktyiqllirekhtnliafytchlpqdlavaqyalflesvtefeqrhhclelakeadldvatitktvv
enirkkdngefshhdlapaldtgtteedrlkidvidwlvfdpaqraealkqgnaimrkflaskkheaakevfvkipqdsi
aeiynqceeqgmesplpaeddnairehlcirayleahetfnewfkhmnsvpqkpalipqptftekvahehkekkyemdf
giwkghldaltadvkekmynvllfvdggwmvdvredakedherthqmvllrklclpmlcfllhtilhstgqyqeclqlad
mvsserhklylvfskeelrkllqklresslmlldqgldplgyeiql

__Pho23p (44 sequences)__

169. Pho23p human (01) XP_057109
msfvecpyhspaerlvaeadeggpsaitgmglcfrcllfsfsgrsgveggrvdlnvfgslglqpwigssrcwggpcssal
rcgwfsswpppsksaipigggsrgagrvsrwppphwleawrvsplplsplspatfgrgfiavavipglwargrgcssdrl
prpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmve
lvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenrenassnhdhddgasgtpk
ekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpk
crgenektmdkalekskkeraynr

170. Pho23p human (02) BAA82887
msfvecpyhspaerlvaeadeggpsaitgmglcfrcllfsfsgrsgveggrvdlnvfgslglqpwigssrcwggpcssal
rcgwfsswpppsksaipigggsrgagrvsrwppphwleawrvsprplsplspxxfgrgfiavavipglwargrgcssdrl
prpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmve
lvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskrsrrqrnnenrenassnhdhddgasgtpk
ekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpk
crgenektmdkalekskkeraynr

171. Pho23p human (03) NP_005528
msfvecpyhspaerlvaeadeggpsaitgmglcfrcllfsfsgrsgveggrvdlnvfgslglqpwigssrcwggpcssal
rcgwfsswpppsksaipigggsrgagrvsrwppphwleawrvsprplsplspatfgrgfiavavipglwargrgcssdrl
prpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmve
lvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenrenassnhdhddgasgtpk
ekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpk
crgenektmdkalekskkeraynr

172. Pho23p human (04) AF181849_1
msfvecpyhspaerlvaeadeggpsaitgmglcfrcllfsfsgrsgveggrvdlnvfgslglqpwigssrcwggpcssal
rcgwfsswpppsksaipigggsrgagrvsrwppphwleawrvsprplsplspatfgrgfiavavipglwargrgcssdrl
prpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmve
lvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenrenassnhdhddgasgtpk
ekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpk
crgenektmdkalekskkeraynr

173. Pho23p human (05) BAB08102
msfvecpyhspaerlvaeadeggpsaitgmglcfrcllfsfsgrsgveggrvdlnvfgslglqpwigssrcwggpcssal
rcgwfsswpppsksaipigggsrgagrvsrwppphwleawrvsprplsplspatfgrgfiavavipglwargrgcssdrl
prpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmve
lvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenrenassnhdhddgasgtpk

ekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpk
crgenektmdkalekskkeraynr

174. Pho23p human (06) AF074968_1
mlyledylemieqlpmdlrdrftemremdlqvqnamdqleqrvseffmnakknkpewreeqmasikkdyykaleda
dekvqlanqiydlvdrhlrkldqelakfkmeleadnagiteilerrsleldtpsqpvnnhhahshtpvekrkynptshhtttdh
ipekkfkseallstltsdaskentlgcrnnnstassnnaynvnssqplgsynigslssgtgagaitmaaaqavqataqmk
egrrtsslkasyeafknndfqlgkefsmaretvgyssssalmttltqnasssaadsrsgrksknnnksssqqssssssss
slsscssssstvvqeisqqttvvpesdsnsqvdwtydpneprycicnqvsygemvgcdnqdcpiewfhygcvglteapkg
kwycpqctaamkrrgsrhk

175. Pho23p human (07) NP_061944
mlyledylemieqlpmdlrdrftemremdlqvqnamdqleqrvseffmnakknkpewreeqmasikkdyykaleda
dekvqlanqiydlvdrhlrkldqelakfkmeleadnagiteilerrsleldtpsqpvnnhhahshtpvekrkynptshhtttdh
ipekkfkseallstltsdaskentlgcrnnnstassnnaynvnssqplgsynigslssgtgagaitmaaaqavqataqmk
egrrtsslkasyeafknndfqlgkefsmaretvgyssssalmttltqnasssaadsrsgrksknnnksssqqssssssss
slssssssstvvqeisqqttvvpesdsnsqvdwtydpneprycicnqvsygemvgcdnqdcpiewfhygcvglteapkg
kwycpqctaamkrrgsrhk

176. Pho23p human (08) BAA90942
mlyledylemieqlpmdlrdrftemremdlqvqnamdqleqrvseffmnakknkpewreeqmasikkdyykaleda
dekvqlanqiydlvdrhlrkldqelakfkmeleadnagiteilerrsleldtpsqpvnnhhahshtpvekrkynptshhtttdh
ipekkfkseallstltsdaskentlgcrnnnstassnnaynvnssqplgsynigslssgtgagaitmaaaqavqataqmk
egrrtsslkasyeafknndfqlgkefsmaretvgyssssalmttltqnasssaadsrsgrksknnnksssqqssssssss
slssssssstvvqeisqqttvvpesdsnsqvdwtydpneprycicnqvsygemvgcdnqdcpiewfhygcvglteapkg
kwycpqctaamkrrgsrhk

177. Pho23p human (09) AAG23285
mlyledylemieqlpmdlrdrftemremdlqvqnamdqleqrvseffmnakknkpewreeqmasikkdyykaleda
dekvqlanqiydlvdrhlrkldqelakfkmeleadnagiteilerrsleldtpsqpvnnhhahshtpvekrkynptshhtttdh
ipekkfkseallstltsdaskentlgcrnnnstassnnaynvnssqplgsynigslssgtgagaitmaaaqavqataqmk
egrrtsslkasyeafknndfqlgkefsmaretvgyssssalmttltqnasssaadsrsgrksknnnksssqqssssssss
slssssssstvvqeisqqttvvpesdsnsqvdwtydpneprycicnqvsygemvgcdnqdcpiewfhygcvglteapkg
kwycpqctaamkrrgsrhk

178. Pho23p human (10) AAC12956
ieqlpmdlrdrftemremdlqvqnamdqleqrvseffmnakknkpewreeqmasikkdyykaledadekvqlanqiy
dlvdrhlrkldqelakfkmeleadnagiteilerrsleldtpsqpvnnhhahshtpvekrkynptshhtttdhipekkfksea
llstltsdaskentlgcrnnnstassnnaynvnssqplgsynigslssgtgagaitmaaaqavqataqmkegrrtsslka
syeafknndfqlgkefsmaretvgyssssalmttltqnasssaadsrsgrksknnnksssqqsssssssslsscssst
vvqeisqqttvvpesdsnsqvdwtydpneprycicnqvsygemvgcdnqdcpiewfhygcvglteapkgkwycpqct
aamkrrgsrhk

179. Pho23p human (11) XP_006980
maagmylehyldsienlpfelqrnfqlmrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgd
dkvqlamqtyemvdkhirrldtdlarfeadlkekqiessdydssskgrtqkekkaararskgknsdeeapktaqkklkl

vrtspeygmpsvtfgsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfcprcs
qerkkk

180. Pho23p human (12) NP_057246
maagmylehyldsienlpfelqrnfqlmrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgd
dkvqlamqtyemvdkhirrldtdlarfeadlkekqiessdydssssskgkkkgrtqkekkaararskgknsdeeapktaqk
klklvrtspeygmpsvtfgsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfc
prcsqerkkk

181. Pho23p human (13) AAD48585
maagmylehyldsienlpfelqrnfqlmrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgd
dkvqlamqtyemvdkhirrldtdlarfeadlkekqiessdydssssskgkkkgrtqkekkaararskgknsdeeapktaqk
klklvrtspeygmpsvtfgsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfc
prcsqerkkk

182. Pho23p human (14) AAH07781
maagmylehyldsienlpfelqrnfqlmrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgd
dkvqlamqtyemvdkhirrldtdlarfeadlkekqiessdydssssskgkkkgrtqkekkaararskgknsdeeapktaqk
klklvrtspeygmpsvtfgsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfc
prcsqerkkk

183. Pho23p human (15) AF156552_1
maagmylehyldsienlpfelqrnfqlmrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgd
dkvqlamqtyemvdkhirrldtdlarfeadlkekqiessdydssssskgkkkgrtqkekkaararskgknsdeeapktaqk
klklvrtspeygmpsvtfgsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfc
prcsqerkkk

184. Pho23p human (16) AAH13038
mrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgddkvqlamqtyemvdkhirrldtdlarf
eadlkekqiessdydssssskgkksrtqkekkaararskgknsdeeapktaqkklklvrtspeygmpsvtfgsvhpsdvld
mpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfcprcsqerkkk

185. Pho23p human (17) AAB60879
mplctatriprysssdpgpvargrgcssdrlprpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdga
qkrrmlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkp
nskrsrrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemig
cdndecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

186. Pho23p human (18) AAG02579
ysssdpgpvgrgrgcssdrlprpagparrqfqaaslltrgwgrawpwkqilkeldecyerfsretdgaqkrrmlhcvqr
alirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnn
enrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiew
fhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

187. Pho23p human (19) AAC00501
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir

sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

188. Pho23p human (20) BAA82886
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir
sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

189. Pho23p human (21) AF149721_1
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir
sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

190. Pho23p human (22) AF181850_1
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir
sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

191. Pho23p human (23) BAB08101
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir
sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

192. Pho23p human (24) AF078835_1
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir
sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

193. Pho23p human (25) AAG12175
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sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

194. Pho23p human (26) CAC38067
mlspangeqlhlvnyvedyldsieslpfdlqrnvslmreidakyqeilkeldecyerfsretdgaqkrrmlhcvqralir
sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

195. Pho23p human (27) AAG02578
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sqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskrsrrqrnnenre
nassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdndecpiewfhfs
cvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

196. Pho23p human (28) BAA82889
ilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgns
gkvgadrpngdavaqsdkpnskrsrrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpid
pneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

197. Pho23p human (29) BAA83462
mlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskr
srrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdnd
ecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

198. Pho23p human (30) BAA83496
mlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskr
srrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdnd
ecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

199. Pho23p human (31) AF149722_1
mlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvgnsgkvgadrpngdavaqsdkpnskr
srrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdnd
ecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

200. Pho23p human (32) AF149723_1
meilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtvg
nsgkvgadrpngdavaqsdkpnskrsrrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadl
pidpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

201. Pho23p human (33) AF063594_1
maagmylehyldsienlpfelqrnfqlmrdldqrtedlkaeidklateymssarslsseeklallkqiqeaygkckefgd
dkvqlamqtyemvdkhirrldtdlarfeadlkekqiessdydssskgkksrtqkekkaararskgknsdeeapktaqkk
lklvrtspeygmpsvtfgsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcsiewfhfacvglttkprgkwfch
aaprteeeidkglgfqhsffhip

202. Pho23p human (34) XP_029280
meilkeldecyerfsretdgaqkrrmlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtag
nsgkagadrpkgeaaaqadkpnskrsrrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlp
idpneptyclcnqvsygemigcdndecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

203. Pho23p human (35) BAB08103
mlhcvqralirsqelgdekiqivsqmvelvenrtrqvdshvelfeaqqelgdtagnsgkagadrpkgeaaaqadkpnskr
srrqrnnenrenassnhdhddgasgtpkekkaktskkkkrskakaereaspadlpidpneptyclcnqvsygemigcdnd
ecpiewfhfscvglnhkpkgkwycpkcrgenektmdkalekskkeraynr

Figure 4

204. Pho23p human (36) NP_115705
matamylehyldsienlpcelqrnfqlmreldqrtedkkaeidilaaeyistvktlspdqrverlqkiqnayskckeysd
dkvqlamqtyemvdkhirrldadlarfeadlkdkmegsdfessggrglkkgrgqkekrgsrgrgrrtseedtpkkkkhkg
gseftdtilsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcpiewfhfacvdlttkpkgkwfcprcvqekrkk
k

205. Pho23p human (37) AF189286_1
matamylehyldsienlpcelqrnfqlmreldqrtedkkaeidilaaeyistvktlspdqrverlqkiqnayskckeysd
dkvqlamqtyemvdkhirrldadlarfeadlkdkmegsdfessggrglkkgrgqkekrgsrgrgrrtseedtpkkkkhkg
gseftdtilsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcpiewfhfacvdlttkpkgkwfcprcvqekrkk
k

206. Pho23p human (38) BAB85078
matamylehyldsienlpcelqrnfqlmreldqrtedkkaeidilaaeyistvktlspdqrverlqkiqnayskckeysd
dkvqlamqtyemvdkhirrldadlarfeadlkdkmegsdfessggrglkkgrgqkekrgsrgrgrrtseedtpkkkkhkg
gseftdtilsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcpiewfhfacvdlttkpkgkwfcprcvqekrkk
k

207. Pho23p human (39) NP_001555
mlgqqqqqlyssaalltgersrlltcyvqdylecveslphdmqrnvsvlreldnkyqetlkeiddvyekykkeddlnqkk
rlqqllqralinsqelgdekiqivtqmlelvenrarqmelhsqcfqdpaeserasdkakmdssqperssrrprrqrtses
rdlchmangiedcddqppkekksksakkkkrskakqereaspvefaidpneptyclcnqvsygemigcdneqcpiewf
hfscvsltykpkgkwycpkcrgdnektmdkstektkkdrrsr

208. Pho23p human (40) BAA36419
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rlqqllqralinsqelgdekiqivtqmlelvenrarqmelhsqcfqdpaeserasdkakmdssqperssrrprrqrtses
rdlchmangiedcddqppkekksksakkkkrskakqereaspvefaidpneptyclcnqvsygemigcdneqcpiewf
hfscvsltykpkgkwycpkcrgdnektmdkstektkkdrrsr

209. Pho23p human (41) AF053537_1
mlgqqqqqlyssaalltgersrlltcyvqdylecveslphdmqrnvsvlreldnkyqetlkeiddvyekykkeddlnqkk
rlqqllqralinsqelgdekiqivtqmlelvenrarqmelhsqcfqdpaeserasdkakmdssqperssrrprrqrtses
rdlchmangiedcddqppkekksksakkkkrskakqereaspvefaidpneptyclcnqvsygemigcdneqcpiewf
hfscvsltykpkgkwycpkcrgdnektmdkstektkkdrrsr

210. Pho23p human (42) AAG11396
mlgqqqqqlyssaalltgersrlltcyvqdylecveslphdmqrnvsvlreldnkyqetlkeiddvyekykkeddlnqkk
rlqqllqralinsqelgdekiqivtqmlelvenrarqmelhsqcfqdpaeserasdkakmdssqperssrrprrqrtses
rdlchmangiedcddqppkekksksakkkkrskakqereaspvefaidpneptyclcnqvsygemigcdneqcpiewf
hfscvsltykpkgkwycpkcrgdnektmdkstektkkdrrsr

211. Pho23p human (43) CAC20567
mlgqqqqqlyssaalltgertrlltcyvqdylecveslphdmqrnvsvlreldnkyqetlkeiddvyekykkeddlnqkk

rlqqllqralinsqelgdekiqivtqmlelvenrarqmelhsqcfqdpaeserasdkakmdssqperssrrprrqrtses
rdlchmangiedcddqppkekksksakkkkrskakqereaspvefaidpneptyclcnqvsygemigcdneqcpiewf
hfscvsltykpkgkwycpkcrgdnektmdkstektkkdrrsr

212. Pho23p human (44) AAH05370
matamylehyldsienlpcelqrnfqlmreldqrtedkkaeidilaaeyistvktlspdqrverlqkiqnayskckeysd
dkvqlamqtyemvdkhirrldadlarfeadlkdkmegsdfessggrglkkgrgqkekrgsrgrgrrtseedtpkkkkhkg
gseftdtilsvhpsdvldmpvdpneptyclchqvsygemigcdnpdcpiewfhfacvdlttkpkgk

Pop2p (18 sequences)

213. Pop2p human (01) NP_004770
mpaalvensqvicevwasnleeemrkireivpsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
ftnekgeypsgintwqfnfkfnltedmysqdsidllansglqfqkheeegidtlhfaellmtsgvvlcdnvkwlsfhsgy
dfgymvklltdsrlpeeeheflhilnlfspsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
mkelffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

214. Pop2p human (02) AAD02685
mpaalvensqvicevwasnleeemrkireivpsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
ftnekgeypsgintwqfnfkfnltedmysqdsidllansglqfqkheeegidtlhfaellmtsgvvlcdnvkwlsfhsgy
dfgymvklltdsrlpeeeheflhilnlfspsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
mkelffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

215. Pop2p human (03) CNT8_HUMAN
mpaalvensqvicevwasnleeemrkireivlsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
ftnekgeypsgintwqfnfkfnltedmysqdsidllansglqfqkheeegidtlhfaellmtsgvvlcdnvkwlsfhsgy
dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
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216. Pop2p human (04) T34529
mpaalvensqvicevwasnleeemrkireivlsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
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dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
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217. Pop2p human (05) CAB59181
mpaalvensqvicevwasnleeemrkireivlsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
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dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
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218. Pop2p human (06) AF180476_1
mpaalvensqvicevwasnleeemrkireivlsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
ftnekgeypsgintwqfnfkfnltedmysqdsidllansglqfqkheeegidtlhfaellmtsgvvlcdnvkwlsfhsgy
dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
mkelffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

219. Pop2p human (07) AAH08916
mpaalvensqvicevwasnleeemrkireivlsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
ftnekgeypsgintwqfnfkfnltedmysqdsidllansglqfqkheeegidtlhfaellmtsgvvlcdnvkwlsfhsgy
dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
mkelffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

220. Pop2p human (08) AAH17366
mpaalvensqvicevwasnleeemrkireivlsysyiamdtefpgvvvrpigefrssidyqyqllrcnvdllkiiqlglt
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dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
mkelffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

221. Pop2p human (09) BAB15119
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ftnekgeypsgintwqfnfkfnltedmysqdsidllansglqfqkheeegidtlhfaellmtsgvvlcdnvrwlsfhsgy
dfgymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffr
mkelffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

222. Pop2p human (10) CNO7_HUMAN
mpaxtvdhsqricevwacnldeemkkirqvirkynyvamdtefpgvvarpigefrsnadyqyqllrcnvdllkiiqlglt
fmneqgeyppgtstwqfnfkfnltedmyaqdsiellttsgiqfkkheeegietqyfaellmtsgvvlcegvkwlsfhsgy
dfgylikiltnsnlpeeeldffeilrlffpviydvkylmkscknlkgglqevaeqlelerigpqhqagsdslltgmaffk
mremffedhiddakycghlyglgsgssyvqngtgnayeeeankqs

223. Pop2p human (11) NP_037486
mkkirqvirkynyvamdtefpgvvarpigefrsnadyqyqllrcnvdllkiiqlgltfmneqgeyppgtstwqfnfkfnl
tedmyaqdsiellttsgiqfkkheeegietqyfaellmtsgvvlcegvkwlsfhsgydfgylikiltnsnlpeeeldffe
ilrlffpviydvkylmkscknlkgglqevaeqlelerigpqhqagsdslltgmaffkmremffedhiddakycghlyglg
sgssyvqngtgnayeeeankqs

224. Pop2p human (12) L46722_1
mkkirqvirkynyvamdtefpgvvarpigefrsnadyqyqllrcnvdllkiiqlgltfmneqgeyppgtstwqfnfkfnl
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ilrlffpviydvkylmkscknlkgglqevaeqlelerigpqhqagsdslltgmaffkmremffedhiddakycghlyglg
sgssyvqngtgnayeeeankqs

225. Pop2p human (13) AAH07315
mpaatvdhsqricevwacnldeemkkirqvirkynyvamdtefpgvvarpigefrsnadyqyqllrcnvdllkiiqlglt
fmneqgeyppgtstwqfnfkfnltedmyaqdsiellttsgiqfkkheeegietqyfaellmisgvvlcegvkwlsfhsgy
dfgylikiltnsnlpeeeldffeilrlffpviydvkylmkscknlkgglqevaeqlelerigpqhqagsdslltgnayee
eankqs

226. Pop2p human (14) XP_005074
mkkihqvirkynyvamdtefpgvvarptggfrsnadyqyqllrcnvdllkiiqlgltfineqgeyppgtstwqfnfkfnl
tedmyaqnsiellttsgiqfkkhdeegietqyfaellmtsgvvlcegvkwlsfhssynfgylikmltnsnlpeeeldffe

ilrlflpviydvkylmksckhlkdglqevaeqlelarigpphqagsksllltgmaffkmrgmffedhtddakycghlyglg
sgssyvqngtgnayeeeankqs

227. Pop2p human (15) NP_473367
mkkirqvirkynyvamdtefpgvvarpigefrsnadyqyqllrcnvdllkiiqlgltfmneqgeyppgtstwqfnfkfnl
tedmyaqdsiellttsgiqfkkheeegietqyfaellmtsgvvlcegvkwlsfhsgydfgylikiltnsnlpeeeldffe
ilrlffpviydvkylmkscknlkgglqevaeqlelerigpqhqagsdslltgmaffkmrev

228. Pop2p human (16) XP_093120
mpaatvhhsqricevwacnvdeemkkihqvirkynyvamdtefpgvvarptggfrsnadyqyqllrcnvdllkiiqlglt
fineqgeyppgtstwqfnfkfnltedmyaqnsiellttsgiqfkkhdeegietqyfaellmtsgvvlcegvkwlsfhssy
nfgylikmltnsnlpeeeldffeilrlflpviydvkylmksckhlkdglqevaeqlela

229. Pop2p human (17) XP_060082
myvklisssghkvivkreyavtsitikamlsgpaatvahspricevwacnldeemkkirqvirkyhyvamvtefpgvvar
pirelrsnpdyqyqllqcnvdflkiiqlgltfmneqgeyppgtstwqlnfkfnlmedmhaqhsiellttsdiqykkh

230. Pop2p human (18) XP_039984
mrresillesilgssisnltlqrtctprisidllansglqfqkheeegidtlhfaellmtsgvvlcdnvkwlsfhsgydf
gymvklltdsrlpeeeheffhilnlffpsiydvkylmkscknlkgglqevadqldlqrigrqhqagsdslltgmaffrmk
elffedsiddakycgrlyglgtgvaqkqnedvdsaqekmsilaiinnmqq

<u>**Puf6p (9 sequences)**</u>

231. Puf6p human (01) BAA02808
mweilrrkdcdkekrvklmsdlqkliqgkiktiafahdstrviqcyiqygneeqrkqafeelrddlvelskakysrnivk
kflmygskpqiaeiirsfkghvrkmlrhaeasaiveyayndkaileqrnmlteelygntfqlyksadhrtldkvlevqpe
klelimdemkqiltpmaqkeavikhslvhkvfldfftyappklrsemieaireavvylahthdgarvamhclwhgtpkdr
kvivktmktyvekvangqyshlvllaafdciddtklvkqiiiseiisslpsivndkygrkvllyllsprdpahtvreiie
vlqkgdgnahskkdtevrrrellesispallsylqehaqevvldksacvlvsdilgsatgdvqptmnaiaslaatglhpg
gkdgelhiaehpaghlvlkwlieqdkkmkengregcfaktlvehvgmknlkswasvnrgaiilsslqscdlevankvka
alksliptlektkstskgieillekist

232. Puf6p human (02) Y020_HUMAN
mweilrrkdcdkekrvklmsdlqkliqgkiktiafahdstrviqcyiqygneeqrkqafeelrddlvelskakysrnivk
kflmygskpqiaeiirsfkghvrkmlrhaeasaiveyayndkaileqrnmlteelygntfqlyksadhrtldkvlevqpe
klelimdemkqiltpmaqkeavikhslvhkvfldfftyappklrsemieaireavvylahthdgarvamhclwhgtpkdr
kvivktmktyvekvangqyshlvllaafdciddtklvkqiiiseiisslpsivndkygrkvllyllsprdpahtvreiie
vlqkgdgnahskkdtevrrrellesispallsylqehaqevvldksacvlvsdilgsatgdvqptmnaiaslaatglhpg
gkdgelhiaehpaghlvlkwlieqdkkmkengregcfaktlvehvgmknlkswasvnrgaiilsslqscdlevankvka
alksliptlektkstskgieillekist

233. Puf6p human (03) NP_055693
mweilrrkdcdkekrvklmsdlqkliqgkiktiafahdstrviqcyiqygneeqrkqafeelrddlvelskakysrnivk
kflmygskpqiaeiirsfkghvrkmlrhaeasaiveyayndkaileqrnmlteelygntfqlyksadhptldkvlelqpe
klelimdemkqiltpmaqkeavikhslvhkvfldfftyappklrsemieaireavvylahthdgarvamhclwhgtpkdr

kvivktmktyvekvangqyshlvllaafdciddtklvkqiiiseiisslpsivndkygrkvllyllsprdpahtvreiie
vlqkgdgnahskkdtevrrrellesispallsylqehaqevvldksacvlvsdilgsatgdvqptmnaiaslaatglhpg
gkdgelhiaehpaghlvlkwlieqdkkmkengregcfaktlvehvgmknlkswasvnrgaiilssllqscdlevankvka
alksliptlektkstskgieilleklst

234. Puf6p human (04) AAH16137
mweilrrkdcdkekrvklmsdlqkliqgkiktiafahdstrviqcyiqygneeqrkqafeelrddlvelskakysrnivk
kflmygskpqiaeiirsfkghvrkmlrhaeasaiveyayndkaileqrnmlteelygntfqlyksadhptldkvlelqpe
klelimdemkqiltpmaqkeavikhslvhkvfldfftyappklrsemieairea vvylahthdgarvamhclwhgtpkdr
kvivktmktyvekvangqyshlvllaafdciddtklvkqiiiseiisslpsivndkygrkvllyllsprdpahtvreiie
vlqkgdgnahskkdtevrrrellesispallsylqehaqevvldksacvlvsdilgsatgdvqptmnaiaslaatglhpg
gkdgelhiaehpaghlvlkwlieqdkkmkengregcfaktlvehvgmknlkswasvnrgaiilssllqscdlevankvka
alksliptlektkstskgieilleklst

235. Puf6p human (05) AF272350_1
rfrkgnfgtrdaetdgpekgdqkgkaspfeedqnrdlkqgddddskingrglpngmdadckdfnrtpgsrqasptevver
lgpntnpseglgplpnptankplveefsnpetqnldameqvgleslqfdypgnqvpmdssgatvglfdynsqqqlfqrtn
altvqqltaaqqqqyalaaaqqphiagvfsaglapaafvpnpyiisaappgtdpytaaglaaaatlagpavvppqyygvp
wgvypanlfqqqaaaaanntasqqaasqaqpgqqqvlragagqrpltpnqgqqgqqaeslaaaaaanptlafgqglatg
mpgyqvlaptayydqtgalvvgpgartglgapvrlmaptpvlissaaaqaaaaaaaggtassltgstnglfrpigtqppqq
qqqqpstnlqsnsfygsssltnssqsssIfshgpgqpgstslgfgsgnslgaaigsalsgfgssggltngsgryisaapg
aeakyrsasstsslfssssqlfppsrlrynrsdimpsgrsrlledfrnnrfpnlqlrdlighivefsqdqhgsrfiqqkl
eratpaerqmvfneilqaayqlmtdvfgnyviqkffefgsldqklalatrirghvlplalqmygcrviqkalesissdqq
semvkeldghvlkcvkdqngnhvvqkciecvqpqslqfiidafkgqvfvlsthpygcrviqrilehctaeqtlpileelh
qhteqlvqdqygnyviqhvlehgrpedkskivseirgkvlalsqhkfasnvvekcvthasraerallidevccqndgphs
alytmmkdqyanyvvqkmidmaepaqrkiimhkirphittlrkytygkhilaklekyylknspdlgpiggppngml

236. Puf6p human (06) BAA19665
efsnpetqnldameqvgleslqfdypgnqvpmdssgatvglfdynsqqqlfqrtnaltvqqltaaqqqqyalaaaqqphi
agvfsaglapaafvpnpyiisaappgtdpytaaglaaaatlagpavvppqyygvpwgvypanlfqqqaaaaanntasqqa
asqaqpgqqqvlragagqrpltpnqgqqgqqaeslaaaaaanptlafgqglatgmpgyqvlaptayydqtgalvvgpgar
tglgapvrlmaptpvlissaaaqaaaaaaaggtassltgstnglfrpigtqppqqqqqqpstnlqsnsfygsssltnssq
ssslfshgpgqpgstslgfgsgnslgaaigsalsgfgssggltngsgryisaapgaeakyrsasstsslfssssqlfpps
rlrynrsdimpsgrsrlledfrnnrfpnlqlrdlighivefsqdqhgsrfiqqkleratpaerqmvfneilqaayqlmtd
vfgnyviqkffefgsldqklalatrirghvlplalqmygcrviqkalesissdqqsemvkeldghvlkcvkdqngnhvvq
kciecvqpqslqfiidafkgqvfvlsthpygcrviqrilehctaeqtlpileelhqhteqlvqdqygnyviqhvlehgrp
edkskivseirgkvlalsqhkfasnvvekcvthasraerallidevccqndgphsalytmmkdqyanyvvqkmidmaep
aqrkiimhkirphittlrkytygkhilaklekyylknspdlgpiggppngml

237. Puf6p human (07) NP_056132
mnhdfqalalesrgmgellptkkfwepddstkdgqkgiflgddewretawgashhsmsqpimvqrrsgqgfhgnsevn
ailsprsesgglgvsmveyvlssspadkldsrfrkgnfgtrdaetdgpekgdqkgkaspfeedqnrdlkqgddddskingr
glpngmdadckdfnrtpgsrqasptevverlgpntnpseglgplpnptankplveefsnpetqnldameqvgleslqfdyp
gnqvpmdssgatvglfdynsqqqlfqrtnaltvqqltaaqqqqyalaaaqqphiagvfsaglapaafvpnpyiisaappg
tdpytaaglaaaatlagpavvppqyygvpwgvypanlfqqqaaaaanntasqqaasqaqpgqqqvlragagqrpltpnq
gqqgqqaeslaaaaaanptlafgqglatgmpgyqvlaptayydqtgalvvgpgartglgapvrlmaptpvlissaaaqaaa

aaaaggtassltgstnglfrpigtqppqqqqqqpstnlqsnsfygssssltnssqssslfshgpgqpgstslgfgsgnslg
aaigsalsgfgssvgssasssatrreslstssdlykrsssslapigqpfynslgfssspspigmplpsqtpghsltppps
lsshgssssIhlggltngsgryisaapgaeakyrsasstsslfssssqlfppsrlrynrsdimpsgrsrlledfrnnrfp
nlqlrdlighivefsqdqhgsrfiqqkleratpaerqmvfneilqaayqlmtdvfgnyviqkffefgsldqklalatrir
ghvlplalqmygcrviqkalesissdqqsemvkeldghvlkcvkdqngnhvvqkciecvqpqslqfiidafkgqvfvlst
hpygcrviqrilehctaeqtlpileelhqhteqlvqdqygnyviqhvlehgrpedkskivseirgkvlalsqhkfasnvv
ekcvthasraerallidevccqndgphsalytmmkdqyanyvvqkmidmaepaqrkiimhkirphittlrkytygkhila
klekyylknspdlgpiggppngml

238. Puf6p human (08) AF315591_1
mnhdfqalalesrgmgellptkkfwepddstkdgqkgiflgddewretawgashhsmsqpimvqrrsgqgfhgnsevn
ailsprsesgglgvsmveyvlsssspadkldsrfrkgnfgtrdaetdgpekgdqkgkaspfeedqnrdlkqgddddskingr
glpngmdadckdfnrtpgsrqasptevverlgpntnpseglgplpnptankplveefsnpetqnldameqvgleslqfdyp
gnqvpmdssgatvglfdynsqqqlfqrtnaltvqqltaaqqqqyalaaaqqphiagvfsaglapaafvpnpyiisaappg
tdpytaaglaaaatlagpavvppqyygvpwgvypanlfqqqaaaaanntasqqaasqaqpgqqqvlragagqrpltpnq
gqqgqqaeslaaaaaanptlafgqglatgmpgyqvlaptayydqtgalvvgpgartglgapvrlmaptpvlissaaaqaaa
aaaaggtassltgstnglfrpigtqppqqqqqqpstnlqsnsfygssssltnssqssslfshgpgqpgstslgfgsgnslg
aaigsalsgfgssvgssasssatrreslstssdlykrsssslapigqpfynslgfssspspigmplpsqtpghsltppps
lsshgssssIhlggltngsgryisaapgaeakyrsasstsslfssssqlfppsrlrynrsdimpsgrsrlledfrnnrfp
nlqlrdlighivefsqdqhgsrfiqqkleratpaerqmvfneilqaayqlmtdvfgnyviqkffefgsldqklalatrir
ghvlplalqmygcrviqkalesissdqqsemvkeldghvlkcvkdqngnhvvqkciecvqpqslqfiidafkgqvfvlst
hpygcrviqrilehctaeqtlpileelhqhteqlvqdqygnyviqhvlehgrpedkskivseirgkvlalsqhkfasnvv
ekcvthasraerallidevccqndgphsalytmmkdqyanyvvqkmidmaepaqrkiimhkirphittlrkytygkhila
klekyylknspdlgpiggppngml

239. Puf6p human (09) AAH24218
mplpsqtpghsltppps1sshgssssIhlggltngsgryisaapgaeakyrsasstsslfssssqlfppsrlrynrsdim
psgrsrlledfrnnrfpnlqlrdlighivefsqdqhgsrfiqqkleratpaerqmvfneilqaayqlmtdvfgnyviqkf
fefgsldqklalatrirghvlplalqmygcrviqkalesissdqqvisemvkeldghvlkcvkdqngnhvvqkciecvqp
qslqfiidafkgqvfvlsthpygcrviqrilehctaeqtlpileelhqhteqlvqdqygnyviqhvlehgrpedkskivs
eirgkvlalsqhkfasnvvekcvthasraerallidevccqndgphsalytmmkdqyanyvvqkmidmaepaqrkiimh
kirphittlrkytygkhilaklekyylknspdlgpiggppngml

Rad52p (3 sequences)

240. Rad52p human (01) NP_002870
msgteeailggrdshpaagggsvlcfgqcqytaeeyqaiqkalrqrlgpeyissrmagggqkvcyieghrvinlanemfg
yngwahsitqqnvdfvdlnkgkfyvgvcafvrvqlkdgsyhedvgygvseglkskalslekarkeavtdglkralrsfgn
algncildkdylrslnklprqlplevdltkakrqdlepsveearynscrpnmalghpqlqqvtspsrpshavipadqdcs
srslsssaveseathqrklrqkqlqqqfrermekqqvrvstpsaekseaappappvthstpvtvsepllekdflagvtqe
liktlednsekwavtpdagdgvvkpssradpaqtsdtlalnnqmvtqnrtphsvchqkpqaksgswdlqtysadqrttgn
weshrksqdmkkrkydpsy

241. Rad52p human (02) A57518
msgteeailggrdshpaagggsvlcfgqcqytaeeyqaiqkalrqrlgpeyissrmagggqkvcyieghrvinlanemfg
yngwahsitqqnvdfvdlnkgkfyvgvcafvrvqlkdgsyhedvgygvseglkskalslekarkeavtdglkralrsfgn

algncildkdylrslnklprqlplevdltkakrqdlepsveearynscrpnmalghpqlqqvtspsrpshavipadqdcs
srslsssaveseathqrklrqkqlqqqfrermekqqvrvstpsaekseaappappvthstpvtvsepllekdflagvtqe
liktlednsekwavtpdagdgvvkpssradpaqtsdtlalnnqmvtqnrtphsvchqkpqaksgswdlqtysadqrttgn
weshrksqdmkkrkydps

242. Rad52p human (03) XP_052349
msgteeailggrdshpaagggsvlcfgqcqytaeeyqaiqkalrqrlgpeyissrmagggqkvcyieghrvinlanemfg
yngwahsitqqnvdfvdlnngkfyvgvcafvrvqlkdgsyhedvgygvseglkskalslekarkeavtdglkralrsfgn
algncildkdylrslnklprqlplevdltkakrqdlepsveearynscrpnmalghpqlqqvtspsrpshavipadqdcs
srslsssaveseathqrklrqkqlqqqfrermekqqvrvstpsaekseaappappvthstpvtvsepllekdflagvtqe
liktlednsekwavtpdagdgvvkpssradpaqtsdtlalnnqmvtqnrtphsvchqkpqaksgswdlqtysadqrttgn
weshrksqdmkkrkydps

Rpa49p (5 sequences)

243. Rpa49p human (01) AAH14331
maaevlpsarwqycgapdgsqravlvqfsngklqspgnmrftlyenkdstnprkrnqrilaaetdrlsyvgnnfgtgalk
cntlcrhfvgilnktsgqmevydaelfnmqplfsdvsveselalesqtktyrekmdscieafgttkqkralntrrmnrvg
neslnravakaaetiidtkgvtalvsdaihndlqddslylppcyddaakpedvykfedllspaeyealqspseafrnvts
eeilkmieenshctfviealkslpsdvesrdrqarciwfldtlikfrahrvvkrksalgpgvphiintkllkhftcltyn
ngrlrnlisdsmkakitayviilalhihdfqidltvlqrdlklsekrmmeiakamrlkiskrkvsvaagseedhklgtls
lplppaqtsdrlakrrkit

244. Rpa49p human (02) NP_071935
maaevlpsarwqycgapdgsqravlvqfsngklqspgnmrftlyenkdstnprkrnqrilaaetdrlsyvgnnfgtgalk
cntlcrhfvgilnktsgqmevydaelfnmqplfsdvsveselalesqtktyrekmdscieafgttkqkralntrrmnrvg
neslnravakaaetiidtkgvtalvsdaihndlqddslylppcyddaakpedvykfedllspaeyealqspseafrnvts
eeilkmieenshctfviealkslpsdvesrdrqarciwfldtlikfrahrvvkrksalgpgvphiintkllkhftcltyn
ngrlrnlisdsmkakitayviilalhihdfqidltvlqrdlklsekrmmeiakamrlkiskrrvsvaagseedhklgtls
lplppaqtsdrlakrrkit (SEQ. ID NO:248)

245. Rpa49p human (03) BAB14579
maaevlpsarwqycgapdgsqravlvqfsngklqspgnmrftlyenkdstnprkrnqrilaaetdrlsyvgnnfgtgalk
cntlcrhfvgilnktsgqmevydaelfnmqplfsdvsveselalesqtktyrekmdscieafgttkqkralntrrmnrvg
neslnravakaaetiidtkgvtalvsdaihndlqddslylppcyddaakpedvykfedllspaeyealqspseafrnvts
eeilkmieenshctfviealkslpsdvesrdrqarciwfldtlikfrahrvvkrksalgpgvphiintkllkhftcltyn
ngrlrnlisdsmkakitayviilalhihdfqidltvlqrdlklsekrmmeiakamrlkiskrrvsvaagseedhklgtls
lplppaqtsdrlakrrkit (SEQ. ID NO:249)

246. Rpa49p human (04) BAB14791
maaevlpsarwqycgapdgsqravlvqfsngklqspgnmrftlyenkdstnprkrnqrilaaetdrlsyvgnnfgtgalk
cntlcrhfvgilnktsgqmevydaelfnmqplfsdvsveselalesqtktyrekmdscieafgttkqkralntrrmnrvg
neslnravakaaetiidtkgvtalvsdaihndlqddslylppcyddaakpedvykfedllspaeyealqspseafrnvts
eeilkmieenshctfviealkslpsdvesrdrqarciwfldtlikfrahrvvkrksalgpgvphiintkllkhftcltyn
ngrlrnlisdsmkakitayviilalhihdfqidltvlqrdlklsekrmmeiakamrlkiskrrvsvaagseedhklgtls
lplppaqtsdrlakrrkit (SEQ. ID NO:250)

247. Rpa49p human (05) AAH01337
maaevlpsarwqycgapdgsqravlvqfsngklqspgnmrftlyenkdstnprkrnqrilaaetdrlsyvgnnfgtgalk cntlcrhfvgilnktsgqmevydaelfnmqplfsdvsveselalesqtktyrekmdscieafgttkqkralntrrmnrvg neslnravakaaetiidtkgvtalvsdaihndlqddslylppcyddaakpedvykfedllspaeyealqspseafrnvts eeilkmieenshctfvienlkslpsdvesrdrqarciwfldtlikfrahrvvkrksalgpgvphiintkllkhftcltyn ngrlrnlisdsmkakitayviilalhihdfqidltvlqrdlklsekrmmeiakamrlkiskrrvsvaagseedhklgtls lplppaqtsdrlakrrkit (SEQ. ID NO:251)

Rpl14ap (12 sequences)

248. Rpl14ap human (01) XP_056681
mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsarqkyvqqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakktrnriiknevkklqkaallkaspkkapgtkgtaaxxaaaaaak vpakkmtaaskkasaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka (SEQ. ID NO:252)

249. Rpl14ap human (02) AAH05134
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallksspkkapgtkgtaaaaaaaaa aaaaaaakvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka (SEQ. ID NO:253)

250. Rpl14ap human (03) P50914
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaakv pakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka (SEQ. ID NO:254)

251. Rpl14ap human (04) AAC16021
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaakv pakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

252. Rpl14ap human (05) NP_003964
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaa akvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

253. Rpl14ap human (06) AAH00606
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaa akvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

254. Rpl14ap human (07) BAB79460
mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaa aaaaakvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

255. Rpl14ap human (08) AAH19651
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk
adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaa
aaaakvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

256. Rpl14ap human (09) AAH09294
Mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqk
adintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaa
aaakvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

257. Rpl14ap human (10) AAH22805
vfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkfphsahqkyvrqawqkad
intkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaaaa
kvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

258. Rpl14ap human (11) JC5954
mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkflhsahqkyvrqawqka
dintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaaa
aaaakvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

259. Rpl14ap human (12) BAA13443
mvfrrfvevgrvayvsfgphagklvaivdvidqnralvdgpctqvrrqampfkcmqltdfilkflhsahqkyvrqawqka
dintkwaatrwakkiearerkakmtdfdrfkvmkakkmrnriiknevkklqkaallkaspkkapgtkgtaaaaaaaaaa
aaaakvpakkitaaskkapaqkvpaqkatgqkaapapkaqkgqkapaqkapapkasgkka

<u>Rpl16bp (24 sequences)</u>

260. Rpl16bp human (01) AAH04900
heaevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsri
fwrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleek
rkekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

261. Rpl16bp human (02) NP_036555
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

262. Rpl16bp human (03) P40429
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

263. Rpl16bp human (04) S29539
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr

kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

264. Rpl16bp human (05) CAA40254
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

265. Rpl16bp human (06) BAA88214
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

266. Rpl16bp human (07) AAH00514
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

267. Rpl16bp human (08) AAH01675
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

268. Rpl16bp human (09) AAH01836
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrgpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

269. Rpl16bp human (10) XP_058602
maevqvlvldgrghllgrlaaivakqvllgrkvvvvcceginisgnfyrnklnylaflrkrmntspsrgpyhfrapsrvf
wrtvrgmlphktkrgqaaldrlkvsdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekr
kekakihyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

270. Rpl16bp human (11) XP_084406
maevqvlvldgrghllgrlativakqvllgrkvvvvrckginisgnfyrnklkylaflrkrmntnpfrrpyhfrapspif
wltvrsmlphktkrgqaaldrlkvfdcipppydkkkrmvvpaalkvvrlkptrkfaylghlahevgwkyhavtatleekr
kekakihyrkkkelislrkqakrnmekktdkytevlkthgllv

271. Rpl16bp human (12) XP_084360
maevqvlvldgrghllgrlaaivakqvllgrkvvvvrceginisgnfyrnklkylaflrkrmntnpsrvpyhfrapsrif
wrtvrgmlphktkrgqaaldrlkvfdgipppydkkkfaylgrlahevgwkyqavtatleekrkekakihyrkkkqlmrlr
kqaeknvekkidkytevlkthgllv

272. Rpl16bp human (13) XP_058601
maevqvlvldgrghllgrlaaivakqvllgrkvvvvcceginisgnfyrnklnylaflrkrmntspsrgpyhfrapsrvf
wrtvrgmlphktkrgqaaldrlkvsdgipppydkkkfaylgrlahevgwkyqavtatleekrkekakihyrkkkqlmrlr
kqaeknvekkidkytevlkthgllv

273. Rpl16bp human (14) XP_063371
mglelpqlggnplelrrrraapvsnavptqallqryylaeyasitalndvdegvapqaseiawlrphsqcsppармlllp
fteavgiwkfgdppgcpcvvsgktpvtymlsptscdseapsgqlwralkfpiedqvqvplckngg1dfvnsldadkiiql
cviygqwrlcedpylhhstcreegsvvtgdklllgrkvvvvrceginisgnfyrnklknlaflgkrmntnpfrsayhfra
psrifwptceaymlrhktkrghasldclkvfdgipppydkkkrmvvpaalkvvrlkptrkfallgrqaqevrwkyqavta
tleekrkekakihywkkkqlmrlrkqaeknvlkthgllv

274. Rpl16bp human (15) XP_058603
mveaiswaawrpswlnrlnylaflrkrmntspsrgpyhfrapsrvfwrtvrgmlphktkrgqaaldrlkvsdgipppydk
kkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekrkekakihyrkkkqlmrlrkqaeknvekkidkyte
vlkthgllv

275. Rpl16bp human (16) XP_084773
maevqvlvldgrghllghlaaivakqvllgrkvvvvcceginisgnfyrnklkylaflrkrmnsnpsrgpyplqapsrif
wqtmrgmpphktkpgqaaldclkvfdgipppydkkkvclsgapgsrgwlevpgsdshpggeeeresqdplpeeetvhe
ametgreergeen

276. Rpl16bp human (17) XP_084774
mveaiswatwrpswlnrlkylaflrkrmnsnpsrgpyplqapsrifwqtmrgmpphktkpgqaaldclkvfdgipppyd
kkkrmvvpaalkvvrlkparkfaylgrlahevgwkyqavtatleekrkekakihyrkkkqfmrlwkqaeknvekkidky
tevlkthgllv

277. Rpl16bp human (18) XP_084405
mveaiswaawrpswlnrnklkylaflrkrmntnpfrrpyhfrapspifwltvrsmlphktkrgqaaldrlkvfdcipppy
dkkkrmvvpaalkvvrlkptrkfaylghlahevgwkyhavtatleekrkekakihyrkkkelislrkqakrnmekktdky
tevlkthgllv

278. Rpl16bp human (19) XP-058541
mntnsyrgsyhfrapsrifwrtvrgmlphktkrgqaaldrlkvfdgipppydkkkrmvvpvalkvvrlkptrkfaylgrl
ahefgwkyqagtatleekrkekakihygkkkqlmrlrkqaeknvekkidkytevlkthglli

279. Rpl16bp human (20) XP_058350
mntnpfrrpyhfrapspifwltvrsmlphktkrgqaaldrlkvfdcipppydkkkrmvvpaalkvvrlkptrkfaylghl
ahevgwkyhavtatleekrkekakihyrkkkelislrkqakrnmekktdkytevlkthgllv

280. Rpl16bp human (21) XP_089619
mpeaekqleylfpkaarrasilegkrtsgtkgpqnkcnvaitgnkleenthktctvddvllrgsggagpsagdrgyllgh
laavvvkqvllgrkvvvrcesvnvsdnfyrnklkypaffrrmstnpdeapqrlpadsagpavrkaqrgqaaldaevfdg
ipppysrktrwavhlkptrefayvgrlaqeagwkyqavtatleekrkekaethyqkkk

281. Rpl16bp human (22) XP_084775
mrgmpphktkpgqaaldclkvfdgipppydkkkrmvvpaalkvvrlkparkfaylgrlahevgwkyqavtatleekrke
kakihyrkkkqfmrlwkqaeknvekkidkytevlkthgllv

282. Rpl16bp human (23) XP_084361

mlphktkrgqaaldrlkvfdgipppydkkkrmvvpaalkvvrlkptrkfaylgrlahevgwkyqavtatleekrkekaki
hyrkkkqlmrlrkqaeknvekkidkytevlkthgllv

283. Rpl16bp human (24) XP_058542
mlphktkrgqaaldrlkvfdgipppydkkkrmvvpvalkvvrlkptrkfaylgrlahefgwkyqagtatleekrkekaki
hygkkkqlmrlrkqaeknvekkidkytevlkthglli

Rpl19bp (15 sequences)

284. Rpl19bp human (01) XP_094358
msmlglqkrpaasvlrygkkkvwldpneaneiasansrqqirklikdgliickpvtvhsqaqcrkntlahrkgrhmgtgk
rkgtanapmpekvtryrdskkinhhmyhslylkvkesvfkdkqilmehihklkadkagkklladqaeacrpktkearkqr
eeclqakkegiintlskdeemkkqklplltvppsryraqrpvninipvkcalplipfppqivflllrvssktaleadidy
egqkpwlkcrffpkapgklpdhppyraqrqiqliqkafdggrstkrgkgflalqnlsfvvnvagtppknggImecapagl
tadthargaciqegwsglrtweiqeslpdfsynilqagfliqegfrdslpratavvssqvqasvsvplaespqpqqlwat
pgrltatgvhqslffclswesetpsaqasppacrapgaasksgrrenprhhstrppemplvslpcickmgaaletlgprl
rrrggeaapprrwpaafgpgapfpcpvpipcaprlrvagtn

285. Rpl19bp human (02) NP_000972
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae
arrsktkearkrreerlqskkeeiiktlskeeetkk

286. Rpl19bp human (03) P14118
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae
arrsktkearkrreerlqakkeeiiktlskeeetkk

287. Rpl19bp human (04) A48992
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae
arrsktkearkrreerlqakkeeiiktlskeeetkk

288. Rpl19bp human (05) CAA45090
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae
arrsktkearkrreerlqakkeeiiktlskeeetkk

289. Rpl19bp human (06) AAB25672
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae
arrsktkearkrreerlqakkeeiiktlskeeetkk

290. Rpl19bp human (07) AAH00530
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae

arrsktkearkrreerlqakkeeiiktlskeeetkk

291. Rpl19bp human (08) AAH13016
msmlrlqkrlassvlrcgkkkvwldpnetneiananansrqqirklikdgliirkpvtvhsrarcrkntlarrkgrhmgigk
rkgtanarmpekvtwmrrmrilrrllrryreskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqae
arrsktkearkrreerlqakkeeiiktlskeeetkk

292. Rpl19bp human (09) XP_093380
msmlrlqkrlassvlccgkkkvwldpnetseiananansrqqmrklikdeliiskpvdspflglmpekdlgppegrhsgigk
rkgtanarmpekvmwilrrllrryceskkidrhmyhslylkvkgnvfknkrilmehihklkadkarkklladqaeaprsk
tkearkhgeerlqakkeeiiktlskeeetkk

293. Rpl19bp human (10) XP_067821
msilrlqkrlassilccgkkkvwldpgetseianvnsrqqirklirdgliilkpvpvhsqaqcwkntlagrkqkgtanar
mpekitwmrrmrilrlllrryceskkidcymyhslylkvkgnvfknkwilrehshklr

294. Rpl19bp human (11) XP_064481
msmlrlqkrlassvlrcgkkkvwldpnktneiananshqqiwklikdgliirkpvtgtanarmpekvtwmkrmrilhlll
rryceskkidrhmyhslylkvqgnvftnkpilmehshklkadkahkklladqaearrpktkearkrseerlqakkeeiik
tlfkeedtkk

295. Rpl19bp human (12) XP_066532
msmlrlqkrlassvlrcgkkkvwldpnktneiananshqqiwklikdgliirkpvtgtanarmpekvtwmkrmrilhlll
rryceskkidrhmyhslylkvqgnvftnkpilmehshklkadkahkklladqaearrpktkearkrseerlqakkeeiik
tlfkeedtkk

296. Rpl19bp human (13) XP_068464
mtkspnnmkktklpmvqlsqfcffwcvrwnmakftrrskqylktslkslprsrtdrrllyqsetppycdvnkmkgtstks
hsnyrerkscmrspflipftaaatamsmlrlqkrlassvlhwgkkkirklikdgliiwkpvtvhsqaqfwkntlahqkgk
hmcigqvtwirrtrilcrllrryheskkidchmyhslylqmkgnvfknkqilmeyirklkagkackklladqaearrskt
kdarkhseerlqakkwemmktlskeedtkk

297. Rpl19bp human (14) XP_067494
mgiskrkgtanaqmpgnvtwmrrmrilcwllrryceskkidhhtyhslylkvkgnvfknkwilmehilklkadkahkkl
qadqakarrsktkearkhhedrlqakeeiiktlskeeetek

298. Rpl19bp human (15) XP_071008
msmltpqkrlissvlhcgekkirklikdglilrhrkpvtvhsraqcwkstlarrkgrhlgieskkidrhmyhslylklkg
nvfkhkriltehshklkadkarkkpladqaeargsktkearklreehlqtkkeeiiktlsqeekakk

<u>Rpl20bp (23 sequences)</u>

299. Rpl20bp human (01) NP_000971
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfgi
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

300. Rpl20bp human (02) Q02543
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfgi
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

301. Rpl20bp human (03) AAC18781
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfgi
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

302. Rpl20bp human (04) AAC62828
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfgi
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

303. Rpl20bp human (05) AAH07512
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfgi
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

304. Rpl20bp human (06) XP_087211
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfekfplrvknfgi
wlrydsrsgthnmyreyrdlttagavtrcyrdmsarhggrahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

305. Rpl20bp human (07) XP_049201
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfri
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

306. Rpl20bp human (08) XP_058516
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfri
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

307. Rpl20bp human (09) XP_084764
mkasgtlreykvvgrclptpkchtpplyrmrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfri
wlrydsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlr
rqhkprfttkrpntff

308. Rpl20bp human (10) XP_066857
mkapgtrleyqvvgrclpapkchtpplyrmrifapnhvvakshfwyfvsqlkklkkssgeivycgqvfekrplrvknfgi
wlrydsrrgthniyreyrdlttagavtkcyrdmgarhrarahsiqirkvediaaskcrrptvkqfhdskikfplphrvlr
rqhkprfttkrpdtff

309. Rpl20bp human (11) AAF74508

mkapgtrleyqvvgrclpapkchtpplyrmrifapnhvvakshfwyfvsqlkklkkssgeivycgqvfekrplrvknfgi
wlrydsrrgthniyreyrdlttagavtkcyrdmgarhrarahsiqirkvediaaskcrrptvkqfhdskikfplphrvlr
rqhkprfttkrpdtff

310. Rpl20bp human (12) XP_088557
mkasgtlreykvvgrrlptpkchtpplyrmrifapnrvvaksrfwyfvsqlkkmkkssgetvycgqvfeksplrvknfgi
wlrcdsrsgthnmyreyrdlttagavtqcyrdmgarhrarahsiqimmveeiaask

311. Rpl20bp human (13) XP_084763
mrifapnhvvaksrfwyfvsqlkkmkkssgeivycgqvfeksplrvknfriwlrydsrsgthnmyreyrdlttagavtqc
yrdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlrrqhkprfttkrpntff

312. Rpl20bp human (14) XP_060535
mkalgtqqeykvvchclptpkchtlplyhmqifapnhvvakfhfwyflsqlkkmkkssgetvncgqvfekyplwvknf
giwlrydsrssthnmyreyrdlttmgavtqcyqdmgtqyraranfiqimkveeiaaskcwwpvvkqfhdskikfllphlv
lchqqkprftrrpntff

313. Rpl20bp human (15) XP_087212
mkasgtlreyklkkmkkssgeivycgqvfekfplrvknfgiwlrydsrsgthnmyreyrdlttagavtrcyrdmsarhgg
rahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlrrqhkprfttkrpntff

314. Rpl20bp human (16) S47353
scrrqvpllvlcvsvkedeevfrgdcllwqvfeksplrvknfgiwlsydsrsgthnmyreyrdlttagavtqcyrdmgar
hrarahsiqimkveeiavskcrrpavkqfhdskikfplphrvlrrqhkprfttkrpntff

315. Rpl20bp human (17) CAA56788
scrrqvpllvlcvsvkedeevfrgdcllwqvfeksplrvknfgiwlsydsrsgthnmyreyrdlttagavtqcyrdmgar
hrarahsiqimkveeiavskcrrpavkqfhdskikfplphrvlrrqhkprfttkrpntff

316. Rpl20bp human (18) XP_088558
mkasgtlreyklkkmkkssgetvycgqvfeksplrvknfgiwlrcdsrsgthnmyreyrdlttagavtqcyrdmgarhra
rahsiqimmveeiaask

317. Rpl20bp human (19) XP_069583
mkasgalkeykvvvslcpppnathcpstaceslrlnhvvaksrfwyfvsqlkkmkmtsgwivycgqvfekvplrvknfs
vwllydsrscthntyreywdlttmgrhrtqahciqimkveeiaankcrratlhhqeaqhlllgagsspreapariicvmai
tvsgsapkrhllspvscrlspslrlvapgspqlvsnns

318. Rpl20bp human (20) AAC16480
Mkasgalkeykvvvslcpppnathcpstaceslrlnhvvaksrfwyfvsqlkkmkmtsgwivycgqvfekvplrvknfs
vwllydsrscthntyreywdlttmgrhrtqahciqimkveeiaankcrratlhhqeaqhlllgagssprvcpk

319. Rpl20bp human (21) XP_066822
mfapnhvvakssfwyfvsqlkkmkkfsgeiaysgwvfeksplrvknfriwlrcdslsgthnlyreyqdlttagghpvlps
hglsalrpgplhpdhegggdrsrqvppavrqavprl

Figure 4

320. Rpl20bp human (22) XP_093371
mtaadqkvkqgsmwyvgfetsflrvknfgiwlgydsqsgthnlyreyrdltpvgavtqcymtgaqhralaqsiqimkrf
qdskiqfplphwvlrhqhkphfttkrsntff

321. Rpl20bp human (23) BAA28596
rdmgarhrarahsiqimkveeiaaskcrrpavkqfhdskikfplphrvlrrqhkprfttkrpntff

__Rpl21bp (44 sequences)__

322. Rpl21bp human (01) XP_058405
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

323. Rpl21bp human (02) NP_000973
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

324. Rpl21bp human (03) XP_040644
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

325. Rpl21bp human (04) P46778
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

326. Rpl21bp human (05) S55913
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

327. Rpl21bp human (06) AAA85655
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

328. Rpl21bp human (07) CAA61582
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

329. Rpl21bp human (08) AAH01603

mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

330. Rpl21bp human (09) AAH07505
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

331. Rpl21bp human (10) BAB79464
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

332. Rpl21bp human (11) 1096939
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefm
a

333. Rpl21bp human (12) XP_087514
mtntkgkrrgtrymfsrpfrkhgviplatymriykkgdivdikgtgtvqkgmphkcyhgktgrvynvtqhavgivvnkq
vkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpappraahfvrtngkepellepipyefma

334. Rpl21bp human (13) AAD04204
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqptppreahfvrtngkepellepipyefma

335. Rpl21bp human (14) AAA93231
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhaagivvne
qvkgkilakrinvriehikhsksrdnflkrvkxddqekxeaqekgtwvqlkrxpappreahfvrtngkepellepipyefm
a

336. Rpl21bp human (15) XP_058216
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpapprvahfvrtngkepellepipyefm
e

337. Rpl21bp human (16) AAA80462
rgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnkqvkgkila
krinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrhpappreahfvrtngkepellepipyefma

338. Rpl21bp human (17) XP_058267
mtntkgkrratrymfsrpfrkhgavplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkcmkendqkkkeakekgtwvqlkfqpappreahfvrtngkepellelipyefm
a

339. Rpl21bp human (18) XP_084296
mtntkgkrratrymfsrpfrkhgavplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkcmkendqkkkeakekgtwvqlkfqpappreahfvrtngkepellelipyefm
a

340. Rpl21bp human (19) XP_058414
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkadivdikgmgtaqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrikvriehikhsksrdsflkhvkendqkkkdakekgtwvqlkrqpappreahfvrtngkqpellepisyefm
a

341. Rpl21bp human (20) XP_084429
mffrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvntqvkgkilakrinvf
iehikhsksrdsflkrmkendqkkkeakekgtwvqlkrqpappreahfvrtngkepellepipyefma

342. Rpl21bp human (21) CAB46381
mtntkgkrrgtrymfsrpfrkhgvvplamymriykkgdivdikgmgtvqkgmshkcyhgktgrvynvpqhavgivv
nkqvkgkilakrinvciehikhsksrdsflkrvkendqkkkeakekvtwvqrkhqpappreaqcvrtngkepelletipye
fma

343. Rpl21bp human (22) XP_059120
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgtgtvqkgmphkcyhgktgrvynvtqhavgivvnkq
vkgkilakrinvriehikhsksrdsflkrvkendpppreahfvrtngkepellepipyefma

344. Rpl21bp human (23) XP_058407
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendpppreahfvrtngkepellepipyefma

345. Rpl21bp human (24) XP_066219
mtntkgkrrgtrymfsrpfrkhgvvplatymqiykkgdivdikgmgtvrkgmprkcyhgktggvysvtqhavgivdkil
akrinvriehikhsksrdsflkrmkendqkkkeakekgtwvqlkhqpappreahfvrtngkepelleptpyefmp

346. Rpl21bp human (25) XP_059885
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqtppreahfvrtngkepellepipyefma

347. Rpl21bp human (26) XP_058759
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendppprvahfvrtngkepellepipyefme

348. Rpl21bp human (27) XP_033654
mfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgtphkcyhgktgrvynviqyaasivvnkqvkgkilakrinvri
ehikhsesrdsflkrvkendqkkreakekgtwvqlkrqpappskahfvrtngkepellepilyefta

349. Rpl21bp human (28) XP_086272
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgtgtvqkgmphkcyhgktgrvynvtqhavgivvnkq
vkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpellepipyefma

350. Rpl21bp human (29) XP_088264
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpellepipyefma

351. Rpl21bp human (30) XP_084396
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpellepipyefma

352. Rpl21bp human (31) XP_086478
mtntkgkrrgtrcmfsrpfrkhgvvplatymrvykkgdivdikgmgtvqkgmphtryhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendpppreahfvrtngkepellepipyefma

353. Rpl21bp human (32) XP_085402
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk
qvkgkilakrinvriehikhsksrdsflkrvkendqkkkeakekgtwvqlkrqpellepipyefme

354. Rpl21bp human (33) XP_088698
mtntkgkrrgtqymfsrpfrkhgvvplatymqiykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhtvgivvn
kqvkgkilakrinvriehikhsksrdsflkrmnendqtppreahfvrtngkepellepilyefma

355. Rpl21bp human (34) XP_039551
mtntkgkrrgtrymfsrpfrkhgvvplatcmriykkvdivdikgmgtvqkgmlrecyhgktgrvcsvtqhavgivvnkq
vkgrilakrinvriehiqhsksqnsflkhvkendqkkkeakekgtwvqlkhqpapsraahfvrtngkepellepipcefma

356. Rpl21bp human (35) XP_058677
mtntkgkrrgtrymfsrpfrkhgvvplatymriykkvdivdvkgmgtvqkgmphkcyhgktgrvysvtqhavgivvn
kqvkgkilakrinvrikhikhsksqdsflkrvkendpppreahfvrtsgkepellepipcefma

357. Rpl21bp human (36) XP_086384
mtntkgkrrgtrymfsrpfrkhgvvplamymriykkgdivdikgmgtvqkgmshkcyhgktgrvynvpqhavgivv
nkqvkgkilakrinvciehikhsksrdsflkrvkendqtppreaqcvrtngkepelletipyefma

358. Rpl21bp human (37) XP_084427
mffrpfrkhgvvplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvntqvkgkilakrinvf
iehikhsksrdsflkrmkendpppreahfvrtngkepellepipyefma

359. Rpl21bp human (38) XP_085992
mtktkgkrrgtrytfsrpfrkhgvvplatymriykkgvivdikgmgtvqkgmphkchhgktgrvynvtqhavgivvnkq
vkskilakrinvriehikhseswdsflkymkendqtppreahfvrtnekepellepipyelma

360. Rpl21bp human (39) XP_058514
mtntkgkrrgtpymfsrpfrkhgvvclatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhtvgivvnk
qvkgkilakrinvriehikhsks

361. Rpl21bp human (40) XP_084760

mtntkgkrrgtpymfsrpfrkhgvvclatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhtvgivvnk qvkgkilakrinvriehikhsks

362. Rpl21bp human (41) XP_058408
mgmgtvqkgmphkcyhgktgrvynvtqhavgivvnkqvkgkilakrinvriehikhsksrdsflkrvkendqkkkeak ekgtwvqlkrqpappreahfvrtngkepellepipyefma

363. Rpl21bp human (42) XP_059121
mgtgtvqkgmphkcyhgktgrvynvtqhavgivvnkqvkgkilakrinvriehikhsksrdsflkrvkendqkkkeake kgtwvqlkrqpappreahfvrtngkepellepipyefma

364. Rpl21bp human (43) XP_087393
mtntkgkrratrymfsrpfrkhgavplatymriykkgdivdikgmgtvqkgmphkcyhgktgrvynvtqhavgivvnk qvkgkilakrinvriehi

__Rpl6ap (24 sequences)__

365. Rpl6ap human (01) AAH20679
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg krvvflkqlasgllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprrqegeifdtekeky eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

366. Rpl6ap human (02) AAH22444
magekvekpdtkekrpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgvgrysrsamysrkamykrkysaa kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg krvvflkqlasgllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

367. Rpl6ap human (03) NP_000961
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg krvvflkqlasgllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

368. Rpl6ap human (04) Q02878
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg krvvflkqlasgllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

369. Rpl6ap human (05) I51803
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg krvvflkqlasgllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

370. Rpl6ap human (06) BAA04491
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa
kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg
krvvflkqlasglllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky
eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

371. Rpl6ap human (07) BAB17292
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa
kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg
krvvflkqlasglllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky
eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

372. Rpl6ap human (08) AAH04138
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa
kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg
krvvflkqlasglllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky
eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

373. Rpl6ap human (09) XP_016700
magekvekpdtkekkpeakkadaggkvkkgnlkakkpkkgkphcsrnpvivrgigrysrsamysrkamykrkysaa
kskvekkkkekvlatvtkpvggdkngstrvvklrkmpryyptedvprkllshskkpfsqhvrklrasitpgtiliiltgrhrgk
rvvflkqlasglllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky
eiteqckieqkavdsqilpkikaipqlqgylrsvvaltngiyphklvf

374. Rpl6ap human (10) AAF99680
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkphcsrnpvlvrgigrysrsamysrkamykrkysaa
kskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrrrgk
nwvvflkqlasglllvtgplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekek
yeiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

375. Rpl6ap human (11) S33714
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkpplqpqpcpsqrnwqvfpichvsrkamykrkysa
akskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg
krvvflkqlasglllvtdlwssievplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky
eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

376. Rpl6ap human (12) CAA49188
magekvekpdtkekkpeakkvdaggkvkkgnlkakkpkkgkpplqpqpcpsqrnwqvfpichvsrkamykrkysa
akskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrklrasitpgtiliiltgrhrg
krvvflkqlasglllvtdlwssievplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekeky
eiteqrkidqkavdsqilpkikaipqlqgylrsvfaltngiyphklvf

377. Rpl6ap human (13) XP_066702
mvfslssrillllerekteevnakpssslvqflaqvfleipveigedlvpslpslcidispindpyqvennetpdvlndle
vgspegskvekkkkekvlalvtksvgsdknggtrvlkllkmtryypiegvprkllshgfsqhgrklrasitpwtiliiltg
chrgkrvvflkqlgsgllpvtgplvfnrvplrrthqkfviatstkihisnvkipkhltgiyfkkqqlqkprhqaseifdt

ekekyeiteqckinqkavdsqslpkikaipqlqgylrsvfapmngiyphklvf

378. Rpl6ap human (14) XP_059836
mpryyptedvprkllshskkpfsqhvrklrasitpgtiliiltgrhrgkrvvflkqlasglllvtgplvlnrvplrrthq
kfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekekyeiteqckieqkavdsqilptngiyphklvf

379. Rpl6ap human (15) XP_059835
magekvekpdtkekkpeakkadaggkvkkgnlkakkpkkgkphcsrnpvivrgigrysrsamysrkamykrkysaa
kskvekkkkekvlatvtkpvggdkngstrvvklrkmpryyptedvprkllshskkpfsqhvrhrgkrvvflkqlasglllvt
gplvlnrvplrrthqkfviatstkidisnvkipkhltdayfkkkklrkprhqegeifdtekekyeiteqckieqkavdsqil
pkikaipqlqgyl

380. Rpl6ap human (16) XP_017483
magekvekpdtkekkpeakkadaggkvqegnlkvkkpkkgkpycshnpvlvrgtgrysrsamysrkamykrkysaa
kskiekkkekvlatvtkpvggdknggtqvvklhkmpryyptedvprkllshskkpfsqhvrklqasitpgtiliiltgchrgk
rvvflkqlasglllvtgplvln

381. Rpl6ap human (17) AAB30819
mysrkamykrkysaakskvekkkkekvlatvtkpvggdknggtrvvklrkmpryyptedvprkllshgkkpfsqhvrk
lrasitpgtiliiltgrhrgkrvvflkqlasglllvtgplvsieflyeehtrnlslplqpksisaivkipkhltdayfkkkk
lrkprhqegeifdtekekyeiteqrkidqklwthkfyqksklflsss

382. Rpl6ap human (18) XP_060259
megeqvekpdtkekkpevkkadaggkvkkgnlkakkpknrkphcsqnpvivrgigryspsamysrkatckrkysavk
skvekqkekfpatitkpagggknggtqvvklckmptyyltedvlskllsqgkkpfsqhmrklgkrviflkqlasgwllvtgp
lvlnqvplqrthqksviatsakidisnkekyeiteqhkidqkavdsqiltkikaipqlqgyl

383. Rpl6ap human (19) XP_060819
mysrkatykrkysatkskvekkkkllatvtkpvsgdknggiwviklhkmpryyptedvpqkllshgkipfswhvrklras
itprtiliilighhrskrvvflkqlasglvgtcdwtsgpqsssstkntpeichctstridisnvktpkhltdayftkkkl
qkprhqegeildtekekyeiteqckidqkaadsqilqkskllnindy

384. Rpl6ap human (20) XP_067252
magenfkrldtkkrleakkadtsgkvkkakspqsaqrklrgnitlgtvliilpghhtgkrvaflkqlgsglllvtgslvl
nqvplpkeskglkasettcyaeaglttsnhrqleiklcgi

385. Rpl6ap human (21) XP_066623
magekvdkpdtkekkpkakksdagskvkkgiarysqsamysrkamykrkysaakskvekkkekvlatvakpiddnk
nsstrlvkllkgpryyptkdmtrkilshvknpfsqhlasdlllmtgplvldrvplqrarwkfviatstkidvsnvkiqkhltdi
yfkkkklqkprhqegeifnterekyeiteqckvdrktvdskilpnsklflssratcdlclp

386. Rpl6ap human (22) XP_068919
mnaikrfqdgklvqnkaycgestpqhftglqpyvvsmdegssgfmrigyehwvlvflilsawipekekyeiaeqpkidq
kavdsqilpkiksipqlqcylrsvfaltngiyphklvf

387. Rpl6ap human (23) XP_091159

mnktdknpcfqkfviaistktgisnvkipkhlidahfekqlqkprhqegeisdtekenyktteqckidqkavdsqivrki
kaipqlqgylrsvfaltngiyphklvf

388. Rpl6ap human (24) XP_069122
mpryystedkpqkllshnknsssqhvkkilvalkqlssglllvtepivlnqfllhgthqkfviatstkidindakitqhl
thvyfkkqpwklrnqkdeildiekekdeiteqckidqkavdlqklpkikiipqlqdyl

Rpp1ap (12 sequences)

389. Rpp1ap human (01) XP_087062
masvsklaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaeekkveakk
eeskesdddmglglfd

390. Rpp1ap human (02) NP_000994
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

391. Rpp1ap human (03) P05386
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

392. Rpp1ap human (04) R6HUP1
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

393. Rpp1ap human (05) AAA36471
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

394. Rpp1ap human (06) AAH03369
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

395. Rpp1ap human (07) AAH07590
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

396. Rpp1ap human (08) BAB79474
masvselaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapaggp
apstaaapaeekkveakkeeseesdddmgfglfd

397. Rpp1ap human (09) XP_061503
mrrnhlarhlqentqsnmrmlaqavhslslipdsgyisevmfqesihqlegrlvrqchqireltdkmetqsmyvselkr
tirtledkvaeieaqqcngiyiwkignefeipgfytgkhryklcmrlhlplptaqrcanyislfvhtmqgeydshlpwpf
qdticltildqsqaprptiprnpkgfgyvtfmhlealrqrtfikddtllvhcevstrfdmdslqregfqpqstdagytek
gldgpelklgctellskkkqtlmqksiphtsphkhvsvvapvplspkivciywalilqsnevtitedkfnnlikaaavtv

epfwpsffakalasvnigsllcnagvgrwlqqpaphkqevlplppllpqlrrgkwkqkkknlrsltrtwalvfltklvl

398. Rpp1ap human (10) XP_090893
masiselaciysalilhdnevtvteykikalikaagvnvepfrpglfakapanvnirslicnvgaggpapaaaeekkmea
kkeefedsdddmgfglsd

399. Rpp1ap human (11) XP_016778
masvsklaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapagrp
apstaaapaeekkveakkeeskesdddmglglfd

400. Rpp1ap human (12) XP_087063
masvsklaciysalilhddevtvtedkinalikaagvnvepfwpglfakalanvnigslicnvgaggpapaagaapagrp
apstaaapaeekkveakkeeskesdddmglglfd

<u>Rps10ap (33 sequences)</u>

401. Rps10ap human (01) NP_001005
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

402. Rps10ap human (02) P46783
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

403. Rps10ap human (03) S55918
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

404. Rps10ap human (04) AAA85660
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

405. Rps10ap human (05) AAH01032
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

406. Rps10ap human (06) AAH01955
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

407. Rps10ap human (07) AAH04334
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

408. Rps10ap human (08) AAH05012
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

409. Rps10ap human (09) 1096944
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

410. Rps10ap human (10) XP_059280
mlmpkknriaihellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgcvkeqfawrhfywyltnegs
qylrdylhlppeivpatlhrsrpetgrprpkglegkrparltrreadrdtyrrcsvppgadkkaeagagsatefqfrgrcgrgr
gqppq

411. Rps10ap human (11) XP_004330
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpailrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

412. Rps10ap human (12) XP_084681
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpailrrsrpetgrprpkglegerparltrgeadrdtyrrsavppgadkkaeagagsatefqfrggfgrgr
gqppq

413. Rps10ap human (13) XP_016113
mlmpkknriaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqflksrgyvkeqfawrhfywyltnegi
qylrdylhlppeivpatlcrsrpetgrprpkgleierptrlargeadrdthr

414. Rps10ap human (14) XP_043294
mlmpkknriaiyellfkkgvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegi
qylhdylhlppeivpatlrrrhpetgrprpkglegeqparltrweadrdtyrqsavppgadkkaesgagsatefqfrggfgcg
hsqlpq

415. Rps10ap human (15) XP_091001
mlmpkknriaiyellfkegamvakkdvytpkqpeladknvpnlhvmkamqslksrgymkeqfawrhfywyltnegi
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416. Rps10ap human (16) XP_016670
mlmpkknriaihellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgcvkeqfawrhfywyltnegs
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fqfrgrcgrgrgqppq

417. Rps10ap human (17) CAC00525
mlmpkknriaihellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgcvkeqfawrhfywyltnegs
qylrdylhlppeivpatlhlppeivpatlhrsrpetgrprpkglegkrparltrreadrdtyrrcsvppgadkkaeagagsate
fqfrgrcgrgrgqppq

418. Rps10ap human (18) XP_040498
mlmpkknwiaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslkcrgyvkehfawrhfywyltnec
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419. Rps10ap human (19) XP_088074
mlmpkknwiaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslkcrgyvkehfawrhfywyltnec
iqylrdylhlppeivpatlrrsrpetgrprpkglymrsavlpgadkkaeagagsatef

420. Rps10ap human (20) XP_083966
mlmpkknwiaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslkcrgyvkehfawrhfywyltnec
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421. Rps10ap human (21) XP_058891
mlmpkknwiaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslkcrgyvkehfawrhfywyltnec
iqylrdylhlppeivpatlrrsrpetgrprpkglymrsavlpgadkkaeagagsatef

422. Rps10ap human (22) XP_067737
mlvpkknhivvyellfkegvvvakkdvhmpkhleladknvpnlhvmkamqslksrgyntehfawrhfywyltnegiq
ylhdylhlpletvpvtlccshpengrpqpkglegerphsyrrsavppgadekaeagagsatkfqfrgrfghgcgqlpq

423. Rps10ap human (23) XP_045401
mnsflrrmvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkehfawrhfywyltnegiqylrdylhlpp
eivpatlprsrpetgrpwpkglyvrsavlpgadkkaeagagsatef

424. Rps10ap human (24) XP_088277
mnsflrrmvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkehfawrhfywyltnegiqylrdylhlpp
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425. Rps10ap human (25) XP_068411
mlmpkknqiatyelifkegvmvakkdvhmpkhpeladknvpnamqslksqgymkehfawrhfycdltkegiqylcd
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426. Rps10ap human (26) XP_092748
mvakdihmpkhlelsdknvsnlpvikamqslksrgyvkaqfawrhfywylpnegiqylrdylhlppeivpatlcrsrpgt
grprpkglkgktlagtncvdsenderlretlemqvreafaenddqelfkcnqagkassnhrrtdksysfrqaiwcacnai
msyglalqglesesvf

427. Rps10ap human (27) BAA25817
riaiyellfkegvmvakkdvhmpkhpeladknvpnlhvmkamqslksrgyvkeqfawrhfywyltnegiqylrdylhl

428. Rps10ap human (28) Q15149
mvagmlmprdqlraiyevlfregvmvakkdrrprslhphvpgvtnlqvmramaslrarglvretfawchffwyltnegia
hlrqylhlppeivaaslqrvrrpvamvmparrtphvqavqgplgsppkrgplpteeqrlyrrkeleevspetpvvpattq
rtlarpgpepapatderdrvqkktstkwvnkhlikaqrhisdlyedlrdghnlisllevlsgdslprekgrmrfhklqnv
qialdylrhrqvklvnirnddiadgnpkltlgliwtiilhfqisdiqvsgqsedmtakeklllwsqrmvegyqglrcdnf
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vdpskshrvpldvacargcldeetsralsepradakaysdpstgepatygelqqrcrpdqltglsllplsekaararqee
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Figure 4

sfsglrspvpasellasgvlsraqfeqlkdgkttvkdlselgsvrtllqgsgclagiyledtkekvsiyeamrrgllrat
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klrdvgayskyltcpktklkisykdaldrsmveegtglrlleaaaqstkgyyspysvsgsgstagsrtgsrtgsragsrr
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429. Rps10ap human (29) XP_092957
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qcslgfcctferkrssvspaapgtaapelaaalmlmprknqiavyellfkqgvmvakegvhlprhpeladknvpnlhimk
amqslksqghreeqfawrhfywhltregiqsihqkaeagagsatkfrgrfdrghgqpcq

430. Rps10ap human (30) CAA91196
mvagmlmprdqlraiyevlfregvmvakkdrrprslhphvpgvtnlqvmramaslrarglvretfawchffwyltnegia
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rtlarpgpepapatderdrvqkktstkwvnkhlikaqrhisdlyedlrdghnlisllevlsgdslprekgrmrfhklqnv
qialdylrhrqvklvnirnddiadgnpkltlgliwtiilhfqisdiqvsgqsedmtakeklllwsqrmvegyqglrcdnf
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aellesrvidrelyqqlqrgersvrdvaevdtvrralrganviagvwleeagqklsiynalkkdllpsdmavalleaqag
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crrddgsgqlllplsdarkltfrglrkqitmeelvrsqvmdeatalqlregltsieevtknlqkflegtsciagvfvdat
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lmercitdpqtglcllplkekkrerktssksssvrkrrvvivdpetgkemsvyeayrkglidhqtylelseqeceweeiti
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431. Rps10ap human (31) XP_064636
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432. Rps10ap human (32) XP_044199
mvakkdvhmpkhpeladknvpnlhvmkamqslksqgymkeqfawrhfywyltnegiqylrdylhlppgdctcyptp

433. Rps10ap human (33) XP_088787
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atefqfrggfg

Scp160p (2 sequences)

434. Scp160p human (01) NP_005327
mssvavltqesfaehrsglvpqqikvatlnseeesdpptykdafpplpekaaclesaqepagawgnkirpikasvitqvf
hvpleerkykdmnqfgegeqakicleimqrtgahlelslakdqglsimvsgkldavmkarkdivarlqtqasatvaipke
hhrfvigkngeklqdlelktatkiqiprpddpsnqikitgtkegiekarhevllisaeqdkraverlevekafhpfiagp
ynrlvgeimqetgtrinipppsvnrteivftgekeqlaqavarikkiyeekkkktttiavevkksqhkyvigpkgnslqe
ilertgvsveippsdsisetvilrgepeklgqaltevyakansftvssvaapswlhrfiigkkgqnlakitqqmpkvhie
ftegedkitlegptedvnvaqeqiegmvkdlinrmdyveinidhkfhrhligksganinrikdqykvsvrippdseksnl
iriegdpqgvqqakrellelasrmenertkdliieqrfhrtiigqkgerireirdkfpeviinfpdpaqksdivqlrgpk
nevekctkymqkmvadlvensysisvpifkqfhkniigkgganikkireesntkidlpaensnsetiiitgkranceaar
srilsiqkdlaniaevevsipaklhnsligtkgrlirsimeecggvhihfpvegsgsdtvvirgpssdvekakkqllhla
eekqtksftvdirakpeyhkfligkgggkirkvrdstgarvifpaaedkdqdlitiigkedavreaqkelealiqnldnv
vedsmlvdpkhhrhfvirrgqvlreiaeeyggvmvsfprsgtqsdkvtlkgakdcveaakkriqeiiedleaqvtlecai
pqkfhrsvmgpkgsriqqitrdfsvqikfpdreenavhstepvvqengdeagegreakdcdpgsprrcdiiisgrkekc
eaakealealvpvtievevpfdlhryvigqkgsgirkmmdefevnihvpapelqsdiiaitglaanldrakagllervke
lqaeqedralrsfklsvtvdpkyhpkiigrkgavitqirlehdvniqfpdkddgnqpqdqititgyeknteaardailri
vgeleqmvsedvpldhrvhariigargkairkimdefkvdirfpqsgapdpncvtvtglpenveeaidhilnleeeylad
vvdsealqvymkppaheeakapsrgfvvrdapwtasssekapdmssseefpsfgaqvapktlpwgpkr

435. Scp160p human (02) AAH14305
gtrapswlhrfiigkkgqnlakitqqmpkvhieftegedkitlegptedvnvaqeqiegmvkdlinrmdyveinidhkfh
rhligksganinrikdqykvsvrippdseksnliriegdpqgvqqakrellelasrmenertkdliieqrfhrtiigqkg
erireirdkfpeviinfpdpaqksdivqlrgpknevekctkymqkmvadlvensysisvpifkqfhkniigkgganikki
reesntkidlpaensnsetiiitgkranceaarsrilsiqkdlaniaevevsipaklhnsligtkgrlirsimeecggvh
ihfpvegsgsdtvvirgpssdvekakkqllhlaeekqtksftvdirakpeyhkfligkgggkirkvrdstgarvifpaae
dkdqdlitiigkedavreaqkelealiqnldnvvedsmlvdpkhhrhfvirrgqvlreiaeeyggvmvsfprsgtqsdkv
tlkgakdcveaakkriqeiiedleaqvtlecaipqkfhrsvmgpkgsriqqitrdfsvqikfpdreenavhstepvvqen
gdeagegreakdcdpgsprrcdiiiisgrkekceaakealealvpvtievevpfdlhryvigqkgsgirkmmdefevnih
vpapelqsdiiaitglaanldrakagllervkelqaeqedralrsfklsvtvdpkyhpkiigrkgavitqirlehdvniq
fpdkddgnqpqdqititgyeknteaardailrivgeleqmvsedvpldhrvhariigargkairkimdefkvdirfpqsg
apdpncvtvtglpenveeaidhilnleeeyladvvdsealqvymkppaheeakapsrgfvvrdapwtasssekapdmsss
eefpsfgaqvapktlpwgpkr

Sdf1p (1 sequence)

436. Sdf1p human (01) CAA16171
mmihgfqsshrdfcfgpwkltaskthimksadvekladelhmpslpemmfgdnvlriqhgsgfgiefnatdalrcvnny
qgmlkvacaeewqesrtegehskevikpydwtyttdykgtllgeslklkvvpttdhidteklkareqikffeevllfedel
hdhgvsslsvkirvmpssffllrfflridgvlirmndtrlyheadktymlreytsreskisslmhvppslftepneisq
ylpikeavceklifperidpnpadsqkstqve

Sec22p (5 sequences)

437. Sec22p human (01) XP_089347
mvlltmiarvadglplaasmqedeqissewhwgnkkiafcgkflnedvffqsgrdlqqyqsqakqlfrklneqsptrctl
eagamtfhyiieqgvcylvlceaafpkklafayledlhsefdeqhgkkvptvsrpysfiefdtfiqktkklyidsrarm
lgsintelqdvqrimvanieevlqrgealsgtqkrcrreaqlspwspgvsqaqsqefsfsysssswvlkaflgkvlmfvs
rlgrkglggtkqqggkektstseartfhrltldtgpetrswrslygfpmshrsyrigglraadkslsgrgsleqpsvstp
qavslpvflrrrvpnkrsttlrsgevllgptkatqvkewmalpqlwlrsplqddillgdghqrqghgrrcqeegvsgfgl
lrqqsthgdaetpektpqdwsprpgsasqaqhsqapgltpgqcgpsprtesgdpggsqhsvrspcgkaaslgchlfsdta
sgrlagrqrlwavtcvqtqrqvalregsvsglspvfrhsvrspcgkaaslgchlfsdtasgrlagrqrlwavtcvqtqrq
valwegsvsglspvfrhsvrspcgkaaslgchlcsdtasgrlagrqrlwavtcvqtqrqvalregsvsglspvfrhsvrs
pcgkaaslgchlcsdtasgrlvgrqrlwavtcvqtqhqvipephtctwaaaplggpslpmgtlcgalswawllpekclpp
sesacvhkaqknrrpqwlprklrntvyarhtsaapptsppaatcksseseelqvathgltqsrawlgteglealgthksr
klpaaltglgflrstl

438. Sec22p human (02) XP_034765
mtfhyiieqgvcdlvlceaafpktlafayledlhsefdeqhgkkvptvsrpysfiefdtfiqktkklyidscarrnlgsi
ntelqdvqrimvanieevlqrgealsaldskannlsslskkyrqdakylnmhstyaklaavavffimlivyvrfwwl

439. Sec22p human (03) NP_036562
msmilsasvirvrdglplsastdyeqstgmqecrkyfkmlsrklaqlpdrctlktghyninfisslgvsymmlctenypn
vlafsfldelqkefittynmmktntavrpycfiefdnfiqrtkqrynnprslstkinlsdmqteiklrppyqismcelgs
angvtsafsvdckgagkissahqrlepatlsgivgfilsllcgalnlirgfhaiesllqsdgddfnyiiafflgtaacly
qcyllvyytgwrnvksfltfglicIcnmylyelrnlwqlffhvtvgafvtlqiwlrqaqgkapdydv

440. Sec22p human (04) XP_087343
msmilsasvirvrdglplsastdyeqstgmqecrkyfkmlsrklaqlpdrctlktghyninfisslgvsymmlctenypn
vlafsfldelqkefittynmmktntavrpycfiefdnfiqrtkqrynnprslstkinlsdmqteiklrppyqismcelgs
angvtsafsvdckgagkissahqrlepatlsgivgfilsllcgalnlirgfhaiesllqsdgddfnyiiafflgtaacly
qvgflpf

441. Sec22p human (05) AAD43013
msmilsasvirvrdglplsastdyeqstgmqecrkyfkmlsrklaqlpdrctlktghynikfisslgvsymmlctenypn
vlafsfldelqkefittynmmktntavrpycfiefnnfiqrtkqrynnprslstkinlsdmqteiklrppyqismcelgs
angvtsafsvdckgagkissahqrlepatlsgivgfilsllcgalnlirgfhaiesllqsdgddfnyiiafflgtaacly
qcyllvyytgwrnvksfltfglicyatcismncatsgsfsfm

Sin3p (3 sequences)

442. Sin3p human (01) AAK95854
mkrrlddqespvyaaqqrripgsteafphqhrvlapappvyeavsetmqsatgiqysvtpsyqvsampqssgshgpaiaa
vhsshhhptavqphggqvvqshahpappvapvqgqqqfqrlkvedalsyldqvklqfgsqpqvyndfldimkefksqsi
dtprvisrvshyskgppilimgiqhlfapwatkmevqtndmvnvttpgqvhqipthgiqpqpqpppqhpsqpsaqsapa

paqpapqpppakvskpsqlqahtpasqqtpplppyasprsppvqphtpvtislgtapslqnnqpvefnhainyvnkiknrf
qgqpdiykafleilhtyqkeqrnakeaggnytpalteqevyaqvarlfknqedllsefgqflpdansfvllskttaekvds
vrndhggtvkkpqlnnkpqrpsqngcqirrhptgttppvkkkpkllnlkdssmadaskhgggteslffdkvrkalrsaea
yenflrclvifnqevisraelvqlvspflgkfpelfnwfknflgykesvhletypkdrategiameidyasckrlgssyr
algksyqqpkctgrtgvckevlndtwvsfpswsedctfvsskktqyeehiyrcederfdlm

443. Sin3p human (02) BAB55197
mkrrlddqespvyaaqqrripgsteafphqhrvlapappvyeavsetmqsatgiqysvtpsyqvsampqssgshgpaiaa
vhsshhhptavqphggqvvqshahpappvapvqgqqqfqrlkvedalsyldqvklqfgsqpqvyndfldimkefksqsi
dtpgvisrvsqlfkghpdlimgfntflppgykievqtndmvnvttpgqvhqipthgiqpqpqpppqhpsqpsaqsapapa
qpapqpppakvskpsqlqahtpasqqtpplppyasprsppvqphtpvtislgtapslqnnqpvefnhainyvnkiknrfqg
qpdiykafleilhtyqkeqrnakeaggnytpalteqevyaqvarlfknqedllsefgqflpdanssvllskttaekvdsv
rndhggtvkkpqlnnkpqrpsqngcqirrhptgttppvkkkpkllnlkdssmadaskhgggteslffdkvrkalrsaeay
enflrclvifnqevisraelvqlvspflgkfpelfnwfknflgykesvhletypkerategiameidyasckrlgssyra
lpksyqqpkctgrtplckevlndtwvsfpswsedstfvsskktqyeehiyrcederfeldvvletnlatirvleaiqkkl
srlsaeeqakfrldntlggtsevihrkalqriyadkaadiidglrknpsiavpivlkrlkmkeeewreaqrgfnkvwreq
nekyylksldhqginfkqndtkvlrskslineiesiyderqeqateenagvpvgphlslayedkqiledaaaliihhvkr
qtgiqkedkykikqimhhfipdllfaqrgdlsdveeeeeeemdvdeatgavkkhngvggsppksklfsntaaqklrgmd
evynlfyvnnnwyifmrlhqilclrllricsqaerqieeenrerewerevlgikrdksdspaiqlrlkepmdvdvedyyp
afldmvrslldgnidssqyedslremftihayiaftmdkliqsivrqlqhivsdeicvqvtdlyla

444. Sin3p human (03) XP_050561
mahagggsggsgaggpagrglsgarwgrsgsagheklpvhvedaltyldqvkirfgsdpatyngfleimkefksqsidtp
gvirrvsqlfhehpdlivgfnaflplgyridipkngklniqspltsqenshnhgdgaedfkqqvpykedkpqvplesdsv
efnnaisyvnkiktrfldhpeiyrsfleilhtyqkeqlntrgrpfrgmseeevftevanlfrgqedllsefgqflpeakr
slftgngpcemhsvqknehdktpehsrkrsrpsllrpvsapakkkmklrgtkdlsiaavgkygtlqefsffdkvrrvlks
qevyenflrcialfnqelvsgsellqlvspflgkfpelfaqfksflgvkelsfappmsdrsgdgisreidyasckrigss
yralpktyqqpkcsgrtaickevlndtwvsfpswsedstfvsskktpyeeqlhrcederfeldvvletnlatirvlesvq
kklsrmapedqekfrlddslggtseviqrraiyriygdkapeiieslkknpvtavpvvlkrlkakeeewreaqqgfnkiw
reqyekaylksldhqavnfkqndtkalrskslineiesvydehqeqhsegrsapssephlifvyedrqiledaaalisyy
vkrqpaiqkedqgtihqllhqfvpslffsqqldlgaseesadedrdspqgqttdpserkkpapgphssppeekgafgdap
ateqpplpppaphkplddvyslffannnwyfflrlhqtlcsrllkiyrqaqkqlleyrtekereklicegrrekgsdpam
elrlkqpseveleeyypafldmvrsllegsidptqyedtlremftihayvgftmdklvqniarqlhhlvsddvclkvvel
ylnekkrgaaggnlssrcvraaretsyqwkaercmadencfkvmflqrkgqvimtielldteeaqtedpvevqhlaryve
qyvgtegassptegfllkpvflqrnlkkfrrrwqseqaralrgearsswkrlvgvesacdvdcrfklsthkmvfivnse
dymyrrgtlcrakqvqplvllrhhqhfeewhsrwlednvtveaaslvqdwlmgeededmvpcktlcetvhvhglpvtry
rvqysrrpasp

__Spt4p (1 sequence)__

445. Spt4p human (01) NP_003159
maletvpkdlrhlracllcslvktidqfeydgcdncdaylqmkgnremvydctsssfdgiiammspedswvskwqrvsn
fkpgvyavsvtgrlpqgivrelksrgvayksrdtaikt

__Sse1p (15 sequences)__

446. Sse1p human (01) NP_006635
msvvgldvgsqscyiavaraggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsnfkrfhgrafndpfi
qkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvpsfftdaerrsvldaa
qivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgtafdpflggknfdekl
vehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqfeelcaellqkievp
lyslleqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspafkvrefsvtdavpf
pisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqnvsaqkdgeksrvkv
kvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdanekkvdqppeakkpkikvvnvelpieanlv
wqlgkdllnmyietegkmimqdklekerndaknaveeyvyefrdklcgpyekficeqdhqnflrllteted wlyeegedq
akqayvdkleelmkigtpvkvrfqeaeerpkmfeelgqrlqhyakiaadfrnkdekynhidesemkkveksvnevme
wmnnvmnaqakksldqdpvvraqeiktkikelnntcepvvtqpkpkiespklertpngpnidkkeedledknnfgaep
phqngecypneknsvnmdld

447. Sse1p human (02) BAA34779
msvvgldvgsqscyiavaraggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsnfkrfhgrafndpfi
qkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvpsfftdaerrsvldaa
qivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgtafdpflggknfdekl
vehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqfeelcaellqkievp
lyslleqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspafkvrefsvtdavpf
pisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqnvsaqkdgeksrvkv
kvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdanekkvdqppeakkpkikvvnvelpieanlv
wqlgkdllnmyietegkmimqdklekerndaknaveeyvyefrdklcgpyekficeqdhqnflrllteted wlyeegedq
akqayvdkleelmkigtpvkvrfqeaeerpkmfeelgqrlqhyakiaadfrnkdekynhidesemkkveksvnevme
wmnnvmnaqakksldqdpvvraqeiktkikelnntcepvvtqpkpkiespklertpngpnidkkeedledknnfgaep
phqngecypneknsvnmdld

448. Sse1p human (03) XP_036357
msvvgldvgsqscyiavaraggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsnfkrfhgrafndpfi
qkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvpsfftdaerrsvldaa
qivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgtafdpflggknfdekl
vehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqfeelcaellqkievp
lyslleqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspafkvrefsvtdavpf
pisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqnvsaqkdgeksrvkv
kvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdknvqqdnseagtqpqvqtdaqqtsqsppspel
tseenkipdadkanekkvdqppeakkpkikvvnvelpieanlvwqlgkdllnmyietevr

449. Sse1p human (04) Q92598
msvvgldvgsqscyiavaraggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsnfkrfhgrafndpfi
qkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvpsfftdaerrsvldaa
qivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgtafdpflggknfdekl
vehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqfeelcaellqkievp
lyslleqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspafkvrefsvtdavpf
pisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqnvsaqkdgeksrvkv
kvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdknvqqdnseagtqpqvqtdaqqtsqsppspel
tseenkipdadkanekkvdqppeakkpkikvvnvelpieanlvwqlgkdllnmyietegkmimqdklekerndaknav
eeyvyefrdklcgpyekficeqdhqnflrllteted wlyeegedqakqayvdkleelmkigtpvkvrfqeaeerpkmfeel

gqrlqhyakiaadfrnkdekynhidesemkkveksvnevmewmnnvmnaqakksldqdpvvraqeiktkikelnntc
epvvtqpkpkiespklertpngpnidkkeedledknnfgaepphqngecypneknsvnmdld

450. Sse1p human (05) AAC18044
rrprpeaeadrepamsvvgldvgsqscyiavaraggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsn
fkrfhgrafndpfiqkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvps
fftdaerrsvldaaqivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgta
fdpflggknfdeklvehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqf
eelcaellqkievplysllеqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspa
fkvrefsvtdavpfpisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqn
vsaqkdgeksrvkvkvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdknvqqdnseagtqpqv
qtdaqqtsqsppspeltseenkipdadkanekkvdqppeakkpkikvvnvelpieanlvwqlgkdllnmyietegkmim
qdklekerndaknaveeyvyefrdklcgpyekficeqdhqnflrlltetedwlyeegedqakqayvdkleelmkigtpvkv
rfqeaeerpkmfeelgqrlqhyakiaadfrnkdekynhidesemkkveksvnevmewmnnvmnaqakksldqdpv
vraqeiktkikelnntcepvvtqpkpkiespklertpngpnidkkeedledknnfgaepphqngecypneknsvnmdld

451. Sse1p human (06) CAA47886
msvvgidlgfqscyvavaraggietianeysdrctpacisfgpknrsigaaaksqvisnakntvqgfkrfhgrafsdpfv
eaeksnlaydivqlptgltgikvtymeeernftteqvtamllsklketaesvlkkpvvdcvvsvpcfytdaerrsvmdat
qiaglnclrlmnettavalaygiykqdlpaleekprnvvfvdmghsayqvsvcafnrgklkvlatafdttlggrkfdevl
vnhfceefgkkykldikskirallrlsqeceklkklmsanasdlplsiecfmndvdvsgtmnrgkflemcndllarvepp
lrsvleqtklkkediyaveivggatripavkekiskffgkelsttlnadeavtrgcalqcailspafkvrefsitdvvpy
pislrwnspaeegssdcevfsknhaapfskvltfyrkepftleayysspsgfalsrsqfsvqkvllslmapvqk

452. Sse1p human (07) NP_055093
msvvgidlgflncyiavarsggietianeysdrctpacislgsrtraignaaksqivtnvrntihgfkklhgrsfddpiv
qterirlpyelqkmpngsagvkvryleeerpfaieqvtgmllaklketsenalkkpvadcvisipsfftdaerrsvmaaa
qvaglnclrlmnettavalaygiykqdlppldekprnvvfidmghsayqvsvcafnkgklkvlattfdpylggrnfdeal
vdyfcdefktkykinvkensrallrlyqeceklkklmsanasdlplniecfmndldvsskmnraqfeqlcasllarvepp
lkavmeqanlqredissieivggatripavkeqitkfflkdisttlnadeavargcalqcailspafkvrefsitdlvpy
sitlrwktsfedgsgecevfcknhpapfskvitfhkkepfeleafytnlhevpypdarigsftiqnvfpqsdgdsskvkv
kvrvnihgifsvasasviekqnlegdhsdapmetetsfknenkdnmdkmqvdqeeghqkchaehtpeeeidhtgakts
avsdkqdrlnqtlkkgkvksidlpiqsslcrqlgqdllnsyienegkmimqdklekerndaknaveeyvydfrdrlgtvye
kfitpedlsklsavledtenwlyedgedqpkqvyvdklqelkkygqpiqmkymeheerpkalndlgkkiqlvmkvieay
rnkderydhldptemekvekcisdamswlnskmnaqnklsltqdpvvkvseivakskeldnfcnpiiykpkpkaevpe
dkpkanserngpmdgqsgtetksdstkdssqhtkssgemevd

453. Sse1p human (08) I56208
msvvgidlgfqscyvavaraggietianeysdrctpacisfgpknrsigaaaksqvisnakntvqgfkrfhgrafsdpfv
eaeksnlaydivqwptgltgikvtymeeernftteqvtamllsklketaesvlkkpvvdcvvsvpcfytdaerrsvmdat
qiaglnclrlmnettavalaygiykqdlprleekprnvvfvdmghsayqvsvcafnrgklkvlatafdttlggrkfdevl
vnhfceefgkkykldikskirallrlsqeceklkklmsanasdlplsiecfmndvdvsgtmnrgkflemcndllarvepp
lrsvleqtklkkediyaveivggatripavkekiskffgkelsttlnadeavtrgcalqcailspafkvrefsitdvvpy
pislrwnspaeegssdcevfsknhaapfskvltfyrkepftleayysspqdlpypdpaiaqfsvqkvtpqsdgssskvkv

kvrvnvhgifsvssaslvevhkseeneepmetdqnakeeekmqvdqeephveeqqqtpaenkaeseemetsqagsk
dkkmdqppqcqegksedqycgpanresaiwqidremlnlyienegkmimqdklekerndaknaveeyvyemrdkls
geyekfvseddrnsftlkledtenwlyedgedqpkqvyvdklaelknlgqpikirfqeseerpnylkn

454. Sse1p human (09) P34932
msvvgidlgfqscyvavaraggietianeysdrctpacisfgpknrsigaaaksqvisnakntvqgfkrfhgrafsdpfv
eaeksnlaydivqlptgltgikvtymeeernftteqvtamllsklketaesvlkkpvvdcvvsvpcfytdaerrsvmdat
qiaglnclrlmnettavalaygiykqdlpaleekprnvvfvdmghsayqvsvcafnrgklkvlatafdttlggrkfdevl
vnhfceefgkkykldikskirallrlsqeceklkklmsanasdlplsiecfmndvdvsgtmnrgkflemcndllarvepp
lrsvleqtklkkediyaveivggatripavkekiskffgkelsttlnadeavtrgcalqcailspafkvrefsitdvvpy
pislrwnspaeegssdcevfsknhaapfskvltfyrkepftleayysspqdlpypdpaiaqfsvqkvtpqsdgssskvkv
kvrvnvhgifsvssaslvevhkseeneepmetdqnakeeekmqvdqeephveeqqqtpaenkaeseemetsqagsk
dkkmdqppqakkakvktstvdlpienqllwqidremlnlyienegkmimqdklekerndaknavreyvyemrdklsg
eyekfvsedgrnsftlkledtenwlyedgedqpkqvyvdklaelknlgqpikirfqeseerpklfeelgkqiqqymkiissfk
nkedqydhldaadmtkvekstneamewmnnklnlqnkqsltmdpvvkskeieakikeltstcspiiskpkpkveppke
eqknaeqngpvdgqgdnpgpqaaeqgtdtavpsdsdkklpemdid

455. Sse1p human (10) BAA75062
msvvgidlgfqscyvavaraggietianeysdrctpacisfgpknrsigaaaksqvisnakntvqgfkrfhgrafsdpfv
eaeksnlaydivqlptgltgikvtymeeernftteqvtamllsklketaesvlkkpvvdcvvsvpcfytdaerrsvmdat
qiaglnclrlmnettavalaygiykqdlpaleekprnvvfvdmghsayqvsvcafnrgklkvlatafdttlggrkfdevl
vnhfceefgkkykldikskirallrlsqeceklkklmsanasdlplsiecfmndvdvsgtmnrgkflemcndllarvepp
lrsvleqtklkkediyaveivggatripavkekiskffgkelsttlnadeavtrgcalqcailspafkvrefsitdvvpy
pislrwnspaeegssdcevfsknhaapfskvltfyrkepftleayysspqdlpypdpaiaqfsvqkvtpqsdgssskvkv
kvrvnvhgifsvssaslvevhkseeneepmetdqnakeeekmqvdqeephveeqqqtpaenkaeseemetsqagsk
dkkmdqppqakkakvktstvdlpienqllwqidremlnlyienegkmimqdklekerndaknavreyvyemrdklsg
eyekfvsedgrnsftlkledtenwlyedgedqpkqvyvdklaelknlgqpikirfqeseerpklfeelgkqiqqymkiissfk
nkedqydhldaadmtkvekstneamewmnnklnlqnkqsltmdpvvkskeieakikeltstcspiiskpkpkveppke
eqknaeqngpvdgqgdnpgpqaaeqgtdtavpsdsdkklpemdid

456. Sse1p human (11) AAA02807
msvvgidlgfqscyvavaraggietianeysdrctpacisfgpknrsigaaaksqvisnakntvqgfkrfhgrafsdpfv
eaeksnlaydivqwptgltgikvtymeeernftteqvtamllsklketaesvlkkpvvdcvvsvpcfytdaerrsvmdat
qiaglnclrlmnettavalaygiykqdlprleekprnvvfvdmghsayqvsvcafnrgklkvlatafdttlggrkfdevl
vnhfceefgkkykldikskirallrlsqeceklkklmsanasdlplsiecfmndvdvsgtmnrgkflemcndllarvepp
lrsvleqtklkkediyaveivggatripavkekiskffgkelsttlnadeavtrgcalqcailspafkvrefsitdvvpy
pislrwnspaeegssdcevfsknhaapfskvltfyrkepftleayysspqdlpypdpaiaqfsvqkvtpqsdgssskvkv
kvrvnvhgifsvssaslvevhkseeneepmetdqnakeeekmqvdqeephveeqqqtpaenkaeseemetsqagsk
dkkmdqppqcqegksedqycgpanresaiwqidremlnlyienegkmimqdklekerndaknaveeyvyemrdkls
geyekfvseddrnsftlkledtenwlyedgedqpkqvyvdklaelknlgqpikirfqeseerpnylkn

457. Sse1p human (12) O95757
msvvgidlgflncyiavarsggietianeysdrctpacislgsrtraignaaksqivtnvrntihgfkklhgrsfddpiv
qterirlpyelqkmpngsagvkvryleeerpfaieqvtgmllaklketsenalkkpvadcvisipsfftdaerrsvmaaa
qvaglnclrlmnettavalaygiykqdlppldekprnvvfidmghsayqvsvcafnkgklkvlattfdpylggrnfdeal
vdyfcdefktkykinvkensrallrlyqeceklkklmsanasdlplniecfmndldvssmnraqfeqlcasllarvepp

lkavmeqanlqredissieivggatripavkeqitkfflkdisttlnadeavargcalqcailspafkvrefsitdlvpy
sitlrwktsfedgsgecevfcknhpapfskvitfhkkepfeleafytnlhevpypdarigsftiqnvfpqsdgdsskvkv
kvrvnihgifsvasasviekqnlegdhsdapmetetsfknenkdnmdkmqvdqeeghqkchaehtpeeeidhtgaktks
avsdkqdrlnqtlkkgkvksidlpiqsslcrqlgqdllnsyienegkmimqdklekerndaknaveeyvydfrdrlgtvye
kfitpedlsklsavledtenwlyedgedqpkqvyvdklqelkkygqpiqmkymeheerpkalndlgkkiqlvmkvieay
rnkderydhldptemekvekcisdamswlnskmnaqnklsltqdpvvkvseivakskeldnfcnpiiykpkpkaevpe
dkpkanserngpmdgqsgtetksdstkdssqhtkssgemevd

458. Sse1p human (13) BAA75063
msvvgidlgflncyiavarsggietianeysdrctpacislgsrtraignaaksqivtnvrntihgfkklhgrsfddpiv
qterirlpyelqkmpngsagvkvryleeerpfaieqvtgmllaklketsenalkkpvadcvisipsfftdaerrsvmaaa
qvaglnclrlmnettavalaygiykqdlppldekprnvvfidmghsayqvsvcafnkgklkvlattfdpylggrnfdeal
vdyfcdefktkykinvkensrallrlyqeceklkklmsanasdlplniecfmndldvsskmnraqfeqlcasllarvepp
lkavmeqanlqredissieivggatripavkeqitkfflkdisttlnadeavargcalqcailspafkvrefsitdlvpy
sitlrwktsfedgsgecevfcknhpapfskvitfhkkepfeleafytnlhevpypdarigsftiqnvfpqsdgdsskvkv
kvrvnihgifsvasasviekqnlegdhsdapmetetsfknenkdnmdkmqvdqeeghqkchaehtpeeeidhtgaktks
avsdkqdrlnqtlkkgkvksidlpiqsslcrqlgqdllnsyienegkmimqdklekerndaknaveeyvydfrdrlgtvye
kfitpedlsklsavledtenwlyedgedqpkqvyvdklqelkkygqpiqmkymeheerpkalndlgkkiqlvmkvieay
rnkderydhldptemekvekcisdamswlnskmnaqnklsltqdpvvkvseivakskeldnfcnpiiykpkpkaevpe
dkpkanserngpmdgqsgtetksdstkdssqhtkssgemevd

459. Sse1p human (14) BAA13192
msvvgldvgsqscyiavararggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsnfkrfhgrafndpfi
qkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvpsfftdaerrsvldaa
qivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgtafdpflggknfdekl
vehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqfeelcaellqkievp
lyslleqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspafkvrefsvtdavpf
pisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqnvsaqkdgeksrvkv
kvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdknvqqdnseagtqpqvqtdaqqtsqsppspel
tseenkipdadkanekkvdqppeakkpkikvvnvelpieanlvwqlgkdllnmyietegkmimqdklekerndaknav
eeyvyefrdklcgpyekficeqdhqnflrllteteddwlyeegedqakqayvdkleelmkigtpvkvrfqeaeerpkmfeel
gqrlqhyakiaadfrnkdekynhidesemkkveksvnevmewmnnvmnaqakksldqdpvvraqeiktkikelnntc
epvvtqpkpkiespklertpngpnidkkeedledknnfgaepphqngecypneknsvnmdld

460. Sse1p human (15) BAA34780
msvvgldvgsqscyiavararggietianefsdrctpsvisfgsknrtigvaaknqqithanntvsnfkrfhgrafndpfi
qkekenlsydlvplknggvgikvmymgeehlfsveqitamlltklketaenslkkpvtdcvisvpsfftdaerrsvldaa
qivglnclrlmndmtavalnygiykqdlpsldekprivvfvdmghsafqvsacafnkgklkvlgtafdpflggknfdekl
vehfcaefktkykldakskirallrlyqeceklkklmssnstdlplniecfmndkdvsgkmnrsqfeelcaellqkievp
lyslleqthlkvedvsaveivggatripavkeriakffgkdisttlnadeavargcalqcailspafkvrefsvtdavpf
pisliwnhdsedtegvhevfsrnhaapfskvltflrrgpfeleafysdpqgvpypeakigrfvvqnvsaqkdgeksrvkv
kvrvnthgiftistasmvekvpteenemsseadmeclnqrppenpdtdknvqqdnseagtqpqvqtdaqqtsqsppspel
tseenkipdadkanekkvdqppeakkpkikvvnvelpieanlvwqlgkdllnmyietegkmimqdklekerndaknav
eeyvyefrdklcgpyekficeqdhqnflrllteteddwlyeegedqakqayvdkleelmkigtpvkvrfqeaeerpkmfeel
gqrlqhyakiaadfrnkdekynhidesemkkveksvnevmewmnnvmnaqakksldqdpvvraqeiktkikelnntc
epvvtqpkpkiespklertpngpnidkkeedledknnfgaepphqngecypneknsvnmdld

Sto1p (10 sequences)

461. Sto1p human (01) NP_002477
msrrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan
ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqddddegfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqiflqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

462. Sto1p human (02) Q09161
msrrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan
ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqddddegfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqiflqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

463. Sto1p human (03) S50082
msrrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan
ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqddddegfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqiflqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

464. Sto1p human (04) CAA56334
msrrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan

ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqddddd egfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqiflqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

465. Stolp human (05) BAA06769
msrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan
ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqdddddegfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqiflqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

466. Stolp human (06) AAH01450
msrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan
ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqdddddegfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqiflqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

467. Stolp human (07) 15988381
ktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllpekltiyttlvgllnarnyn
fggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeedvpqvrrdwyvyaflsslpw
vgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqklkkdrwqerhilrpylafdsi
lcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhciikshwkerktcaaqlvsy
pgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlymrldtmnttcvdrfinwfsh
hlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpsnptciykygdessnslpghs
valclavafkskatndeifsilkdvpnpnqdddddegfsfnplkievfvqtllhlaaksfshsfsalakfhevfktlaes
degklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvweilhstirkmnkhvlkiqkel
eeakeklarqhdgvleeqierlqekvesaqseqknlflvifqrfimiltehlvrcetdgtsvltpwykncierlqqiflq
hhqiiqqymvtlenllftaeldphilavfqqfcalqa

468. Stolp human (08) 15988383
ktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllpekltiyttlvgllnarnyn
fggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeedvpqvrrdwyvyaflsslpw
vgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqklkkdrwqerhilrpylafdsi
lcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhciikshwkerktcaaqlvsy

pgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlymrldtmnttcvdrfinwfsh
hlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpsnptciykygdessnslpghs
valclavafkskatndeifsilkdvpnpnqddddd egfsfnplkievfvqtllhlaaksfshsfsalakfhevfktlaes
degklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvweilhstirkmnkhvlkiqkel
eeakeklarqhdgvleeqierlqekvesaqseqknlflvifqrfimiltehlvrcetdgtsvltpwykncierlqqiflq
hhqiiqqymvtlenllftaeldphilavfqqfcalqa

469. Sto1p human (09) 15988385
ktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllpekltiyttlvgllnarnyn
fggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeedvpqvrrdwyvyaflsslpw
vgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqklkkdrwqerhilrpylafdsi
lcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhciikshwkerktcaaqlvsy
pgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlymrldtmnttcvdrfinwfsh
hlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpsnptciykygdessnslpghs
valclavafkskatndeifsilkdvpnpnqddddd egfsfnplkievfvqtllhlaaksfshsfsalakfhevfktlaes
degklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvweilhstirkmnkhvlkiqkel
eeakeklarqhdgvleeqierlqekvesaqseqknlflvifqrfimiltehlvrcetdgtsvltpwykncierlqqiflq
hhqiiqqymvtlenllftaeldphilavfqqfcalqa

470. Sto1p human (10) A54748
msrrrhsdendggqphkrrktsdanetedhleslickvgeksacslesnleglagvleadlpnykskilrllctvarllp
ekltiyttlvgllnarnynfggefveamirqlkeslkannyneavylvrflsdlvnchviaapsmvamfenfvsvtqeed
vpqvrrdwyvyaflsslpwvgkelyekkdaemdrifantesylkrrqkthvpmlqvwtadkphpqeeyldclwaqiqkl
kkdrwqerhilrpylafdsilcealqhnlppftppphtedsvypmprvifrmfdytddpegpvmpgshsverfvieenlhc
iikshwkerktcaaqlvsypgknkiplnyhivevifaelfqlpapphidvmyttllielcklqpgslpqvlaqatemlym
rldtmnttcvdrfinwfshhlsnfqfrwswedwsdclsqdpespkpkfvrevlekcmrlsyhqrildivpptfsalcpan
ptciykygdessnslpghsvalclavafkskatndeifsilkdvpnpnqddddd egfsfnplkievfvqtllhlaaksfs
hsfsalakfhevfktlaesdegklhvlrvmfevwrnhpqmiavlvdkmirtqivdcaavanwifsselsrdftrlfvwei
lhstirkmnkhvlkiqkeleeakeklarqhkrrsddddrssdrkdgvleeqierlqekvesaqseqknlflvifqrfimi
ltehlvrcetdgtsvltpwykncierlqqifdqhhqiiqqymvtlenllftaeldphilavfqqfcalqa

__Vph1p (7 sequences)__

471. Vph1p human (01) Q93050
mgelfrseemtlaqlflqseaayccvselgelgkvqfrdlnpdvnvfqrkfvnevrrceemdrklrfvekeirkanipim
dtgenpevpfprdmidleanfekienelkeintnqealkrnfleltelkfilrktqqffdemadpdlleesssllepsem
grgtplrlgfvagvinreriptfermlwrvcrgnvflrqaeienpledpvtgdyvhksvfiiffqgdqlknrvkkicegf
raslypcpetpqerkemasgvntriddlqmvlnqtedhrqrvlqaaaknirvwfikvrkmkaiyhtlnlcnidvtqkcli
aevwcpvtdldsiqfalrrgtehsgstvpsilnrmqtnqtpptynktnkftygfqnivdaygigtyreinpapytiitfp
flfavmfgdfghgilmtlfavwmvlresrilsqknenemfstvfsgryiillmgvfsmytgliyndcfskslnifgssws
vrpmftynwteetlrgnpvlqlnpalpgvfggpypfgidpiwniatnkltflnsfkmkmsvilgiihmlfgvslslfnhi
yfkkplniyfgfipeiifmtslfgylvilifykwtaydahtsenapsllihfinmflfsypesgysmlysgqkgiqcflv
vvallcvpwmllfkplvlrrqylrrkhlgtlnfggirvgngpteedaeiiqhdqlsthsedadefdfgdtmvhqaihtie
yclgcisntasylrlwalslahaqlsevlwtmvihiglsvkslagglvlffftafatltvaillimeglsaflhalrlh
wvefqnkfysgtgfkflpfsfehiregkfee

472. Vph1p human (02) CAA96077
mgelfrseemtlaqlflqseaayccvselgelgkvqfrdlnpdvnvfqrkfvnevrrceemdrklrfvekeirkanipim
dtgenpevpfprdmidleanfekienelkeintnqealkrnfleltelkfilrktqqffdemadpdlleessllepsem
grgtplrlgfvagvinreriptfermlwrvcrgnvflrqaeienpledpvtgdyvhksvfiiffqgdqlknrvkkicegf
raslypcpetpqerkemasgvntriddlqmvlnqtedhrqrvlqaaaknirvwfikvrkmkaiyhtlnlcnidvtqkcli
aevwcpvtdldsiqfalrrgtehsgstvpsilnrmqtnqtpptynktnkftygfqnivdaygigtyreinpapytiitfp
flfavmfgdfghgilmtlfavwmvlresrilsqknenemfstvfsgryiillmgvfsmytgliyndcfskslnifgssws
vrpmftynwteetlrgnpvlqlnpalpgvfggpypfgidpiwniatnkltflnsfkmkmsvilgiihmlfgvslslfnhi
yfkkplniyfgfipeiifmtslfgylvilifykwtaydahtsenapsllihfinmflfsypesgysmlysgqkgiqcflv
vvallcvpwmllfkplvlrrqylrrkhlgtlnfggirvgngpteedaeiiqhdqlsthsedadefdfgdtmvhqaihtie
yclgcisntasylrlwalslahahvsevlwtmvihiglsvkslagglvlffffafatltvaillimeglsaflhalrlh
wvefqnkfysgtgfkflpfsfehiregkfee

473. Vph1p human (03) NP_065683
masvfrseemclsqlflqveaayccvaelgelglvqfkdlnmnvnsfqrkfvnevrrceslerilrfledemqneivvql
lekspltplpremitletvleklegelqeanqnqqalkqsfleltelkyllkktqdffetetnladdfftedtsgllelk
avpaymtgklgfiagvinrermasferllwricrgnvylkfsemdapledpvtkeeiqknifiifyqgeqlrqkikkicd
gfratvypcpepaverremlesvnvrledlitvitqteshrqrllqeaaanwhswlikvqkmkavyhilnmcnidvtqqc
viaeiwfpvadatrikraleqgmelsgssmapimttvqsktapptfnrtnkftagfqnivdaygvgsyreinpapytiit
fpflfavmfgdcghgtvmllaalwmilnerrllsqktdneiwntffhgrylillmgifsiytgliyndcfskslnifgss
wsvqpmfrngtwnthvmeeslylqldpaipgvyfgnpypfgidpiwnlasnkltflnsykmkmsvilgivqmvfgvils
lfnhiyfrrtlniilqfipemifilclfgylvfmiifkwccfdvhvsqhapsilihfinmflnysdssnaplykhqqevq
sffvvmalisvpwmllikpfilrashrksqlqasriqedateniegdssspssrsgqrtsadthgalddhgeefnfgdvf
vhqaihtieyclgcisntasylrlwalslahaqlsevlwtmvmnsglqtrgwggivgvfiifavfavltvaillimegls
aflhalrlhwvefqnkfyvgdgykfspfsfkhildgtaee

474. Vph1p human (04) XP_006568
mgslfrsetmclaqlflqsgtayeclsalgekglvqfrdlnqnvssfqrkfvgevkrceelerilvylvqeinradiplp
egeasppapplkqvlemqeqlqklevelrevtknkeklrknllelieythmlrvtktfvkrnvefeptyeefpslesdsl
ldyscmqrlgaklgfvsglinqgkveafekmlwrvckgytivsyaeldesledpetgevikwyvflisfwgeqighkvkk
icdcyhchvypypntaeerreiqeglntriqdlytvlhktedylrqvlckaaesvysrviqvkkmkaiyhmlnmcsfdvt
nkcliaevwcpeadlqdlrraleegsresgatipsfmniiptketpptrirtnkftegfqnivdaygvgsyrevnpalft
iitfpflfavmfgdfghgfvmflfalllvlnenhprlnqsqeimrmffngryilllmglfsvytgliyndcfsksvnlfg
sgwnvsamyssshppaehkkmvlwndsvvrhnsilqldpsipgvfrgpyplgidpiwnlatnrltflnsfkmkmsvilgi
ihmtfgvilgifnhlhfrkkfniylvsipellfmlcifgylifmifykwlvfsaetsrvapsiliefinmflfpasktsg
lytgqeyvqrvllvvtalsvpvlflgkplfllwlhngrscfgvnrsgytlirkdseeevsllgsqdieegnhqvedgcre
maceefnfgeilmtqvihsieyclgcisntasylrlwalslahaqlsdvlwamlmrvglrvdttygvllllpvialfavl
tifillimeglsaflhairlhwvefqnkfyvgagtkfvpfsfsllsskfnnddsva

475. Vph1p human (05) NP_036595
mgslfrsetmclaqlflqsgtayeclsalgekglvqfrdlnqnvssfqrkfvgevkrceelerilvylvqeinradiplp
egeasppapplkqvlemqeqlqklevelrevtknkeklrknllelieythmlrvtktfvkrnvefeptyeefpslesdsl
ldyscmqrlgaklgfvsglinqgkveafekmlwrvckgytivsyaeldesledpetgevikwyvflisfwgeqighkvkk
icdcyhchvypypntaeerreiqeglntriqdlytvlhktedylrqvlckaaesvysrviqvkkmkaiyhmlnmcsfdvt
nkcliaevwcpeadlqdlrraleegsresgatipsfmniiptketpptrirtnkftegfqnivdaygvgsyrevnpalft

iitfpflfavmfgdfghgfvmflfallwvlnenhprlnqsqeimrmffngryillllmglfsvytgliyndcfsksvnlfg
sgwnvsamyssshppaehkkmvlwndsvvrhnsilqldpsipgvfrgpyplgidpiwnlatnrltflnsfkmkmsvilgi
ihmtfgvilgifnhlhfrkkfniylvsipellfmlcifgylifmifykwlvfsaetsrvapsiliefinmflfpasktsg
lytgqeyvqrvllvvtalsvpvlflgkplfllwlhngrscfgvnrsgytlirkdseeevsllgsqdieegnhqvedgcre
maceefnfgeilmtqvihsieyclgcisntasylrlwalslahaqlsdvlwamlmrvglrvdttygvllllpvialfavl
tifillimeglsaflhairlhwvefqnkfyvgagtkfvpfsfsllsskfnnddsva

476. Vph1p human (06) NP_005168
mgelfrseemtlaqlflqseaayccvselgelgkvqfrdlnpdvnvfqrkfvnevrrceemdrklrfvekeirkanipim
dtgenpevpfprdmidleanfekienelkeintnqealkrnfleltelkfilrktqqffdemadpdlleessslleps em
grgtplrlgfvagvinreriptfermlwrvcrgnvflrqaeienpledpvtgdyvhksvfiiffqgdqlknrvkkicegf
raslypcpetpqerkemasgvntriddlqmvlnqtedhrqrvlqaaaknirvwfikvrkmkaiyhtlnlcnidvtqkcli
aevwcpvtdldsiqfalrrgtehsgstvpsilnrmqtnqtpptynktnkftygfqniivdaygigtyreinpapytiitfp
flfavmfgdfghgilmtlfavwmvlresrilsqknenemfstvfsgryiillmgvfsmytgliyndcfskslnifgssws
vrpmftynwteetlrgnpvlqlnpalpgvfggpypfgidpiwniatnkltflnsfkmkmsvilgiihmlfgvslslfnhi
yfkkplniyfgfipeiifmtslfgylvilifykwtaydahtsenapsllihfinmflfsypesgysmlysgqkgiqcflv
vvallcvpwmllfkplvlrrqylrrkhlgtlnfggirvgngpteedaeiiqhdqlsthsedadefdfgdtmvhqaihtie
yclgcisntasylrlwalslahaqlsevlwtmvihiglsvkslagglvlffftafatltvaillimeglsaflhalrlh
wvefqnkfysgtgfkflpfsfehiregkfee

477. Vph1p human (07) AAL77442
mgelfrseemtlaqlflqseaayccvselgelgkvqfrdlnpdvnvfqrkfvnevrrceemdrklrfvekeirkanipim
dtgenpevpfprdmidleanfekienelkeintnqealkrnfleltelkfilrktqqffdemadpdlleessslleps em
grgtplrlgfvagvinreriptfermlwrvcrgnvflrqaeienpledpvtgdyvhksvfiiffqgdqlknrvkkicegf
raslypcpetpqerkemasgvntriddlqmvlnqtedhrqrvlqaaaknirvwfikvrkmkaiyhtlnlcnidvtqkcli
aevwcpvtdldsiqfalrrgtehsgstvpsilnrmqtnqtpptynktnkftygfqnivdaygigtyreinpapytiitfp
flfavmfgdfghgilmtlfavwmvlresrilsqknenemfstvfsgryiillmgvfsmytgliyndcfskslnifgssws
vrpmftynwteetlrgnpvlqlnpalpgvfggpypfgidpiwniatnkltflnsfkmkmsvilgiihmlfgvslslfnhi
yfkkplniyfgfipeiifmtslfgylvilifykwtaydahtsenapsllihfinmflfsypesgysmlysgqkgiqcflv
vvallcvpwmllfkplvlrrqylrrkhlgtlnfggirvgngpteedaeiiqhdqlsthsedadefdfgdtmvhqaihtie
yclgcisntasylrlwalslahahvsevlwtmvihiglsvkslagglvlffftafatltvaillimeglsaflhalrlh
wvefqnkfysgtgfkflpfsfehiregkfee

<u>**Vps9p (5 sequences)**</u>

478. Vps9p human (01) NP_055319
mslkserrgihvdqsdllckkgcgyygnpawqgfcskcwreeyhkarqkqiqedwelaerlqreeeeafassqssqgaqs
ltfskfeekktnektrkvttvkkffsassrvgskkeiqeakapspsinrqtsietdrvskefieflktfhktgqeiykqt
klflegmhykrdlsieeqsecaqdfyhnvaermqtrgkvppervekimdqiekyimtrlykyvfcpettddekkdlaiqk
riralrwvtpqmlcvpvnedipevsdmvvkaitdiiemdskrvprdklacitkcskhifnaikitknepasaddflptli
yivlkgnpprlqsniqyitrfcnpsrlmtgedgyyftnlccavafiekldaqslnlsqedfdrymsgqtsprkqeaesws
pdaclgvkqmyknldllsqlnerqerimneakklekdlidwtdgiarevqdivekypleikppnqplaaidsenvendkl
ppplqpqvyag

479. Vps9p human (02) T12506
eiagaaaenmlgsllclpgsgsvlldpctgstisettseawsvevlpsdseapdlkqeerlqelescsglgstsddtdvr

evssrpstpglsvvsgisatsedipnkiedlrsecssdfggkdsvtspdmdeithdflyilqpkqhfqhieaeadmriql sssahqltsppsqsesllamfdplsshegasavvrpkvhyarpshpppdppilegavggnearlpnfgshvltpaemeaf kqrhsyperlvrsrssdivssvrrpmsdpswnrrpgneerelppaaaigatslvaaphsssssspskdssrgeteerkdsd deksdrnrpwwrkrfvsampkapipfrkkekqekdkddlgpdrfstltddpsprlsaqaqvaedildkyrnaikrtspsd gamanyestevmgdgesahdsprdealqnisaddlpdsasqaahpqdsafsyrdakkklrlalcsadsvafpvlthstrn glpdhtdpedneivcflkvqiaeainlqdknlmaqlqetmrcvcrfdnrtcrkllasiaedyrkrapyiayltrcrqglq ttqahlerllqrvlrdkevanryfttvcvrllleskekkirefiqdfqkltaaddktaqvedflqflygamaqdviwqna seeqlqdaqlaiersvmnrifklafypnqdgdilrdqvlhehiqrlskvvtanhralqipevylreapwpsaqseirtis ayktprdkvqcilrmcstimnllslanedsvpgaddfvpvlvfvlikanppcllstvqyissfyasclsgeesywwmqft aavefiktiddrk

480. Vps9p human (03) XP_044196
mvkldihtlahhlkqerlyvnsekqliqrlnadvlktaeklyrtawiakqqrinldrliitsaeaspaeccqhakiledt qfvdgykqlgfqetaygeflsrlrenprliasslvageklnqentqsviytvftslygncimqedesyllqvlryliefe lkesdnprrllrrgtcafsilfklfseglfsaklfltatlhepimqllvededhletdpnklierfspsqqeklfgekgs drfrqkvqemvesneaklvalvnkfigylkqntycfphslrwivsqmyktlscvdrlevgevramctdlllacficpavv npeqygiisdapinevarfnlmqvgrllqqlamtgseegdprtksslgkfdkscvaafldvviggravetpplssvnlle glsrtvvyitysqlitlvnfnksvmsgdqlredrmaldnllanlppakpgkssslemtpyntpqlspattpankknrlpi atrsrsrtnmlmdlhmdhegssqetiqevqpeevlvislgtgpqltpgmmsenevlnmqlsdggqgdvpvdenklhgk pdktlrfslcsdnlegisegpsnrsnsvssldlegesvselgagpsgsngvealqllehegattqdnlddklrkfeirdmmg ltddrdisetvsetwstdvlgsdfdpnidedrlqeiagaaaenmlgsllclpgsgsvlldpctgstisettseawsvevl psdseapdlkqeerlqelescsglgstsddtdvrevssrpstpglsvvsgisatsedipnkiedlrsecssdfggkdsvt spdmdeithgahqltsppsqsesllamfdplsshegasavvrpkvhyarpshpppdppilegavggnearlpnfgshvlt paemeafkqrhsyperlvrsrssdivssvrrpmsdpswnrrpgneerelppaaaigatslvaaphsssssspskdssrget eerkdsddeksdrnrpwwrkrfvsampkddpsprlsaqaqvaedildkyrnaikrtspsdgamanyestevmgdgesa hdsprdealqnisaddlpdsasqaahpqdsafsyrdakkklrlalcsadsvafpvlthstrnglpdhtdpedneivcflkvq iaeainlqdknlmaqlqetmrcvcrfdnrtcrkllasiaedyrkrapyiayltrcrqglqttqahlerllqrvlrdkeva nryfttvcvrllleskekkirefiqdfqkltaaddktaqvedflqflygamaqdviwqnaseeqlqdaqlaiersvmnri fklafypnqdgdilrdqvlhehiqrlskvvtanhralqipevylreapwpsaqseirtisayktprdkvqcilrmcstim nllslanedsvpgaddfvpvlvfvlikanppcllstvqyissfyasclsgeesywwmqftaavefiktiddrk

481. Vps9p human (04) AAH13635
eafkqrhsyperlvrsrssdivssvrrpmsdpswnrrpgneerelpsaaaigatslvaaphsssssspskdssrgeteerk dsddeksdrnrpwwrkrfvsampkddpsprlsaqaqvaedildkyrnaikrtspsdgamanyestevmgdgesahdsp rdealqnisaddlpdsasqaahpqdsafsyrdakkklrlalcsadsvafpvlthstrnglpdhtdpedneivcflkvqiaea inlqdknlmaqlqetmrcvcrfdnrtcrkllasiaedyrkrapyiayltrcrqglqttqahlerllqrvlrdkevanryf ttvcvrllleskekkirefiqdfqkltaaddktaqvedflqflygamaqdviwqnaseeqlqdaqlaiersvmnrifkla fypnqdgdilrdqvlhehiqrlskvvtanhralqipevylreapwpsaqseirtisayktprdkvqcilrmcstimnlls lanedsvpgaddfvpvlvfvlikanppcllstvqyissfyasclsgeesywwmqftaavefiktiddrk (SEQ ID NO:485)

482. Vps9p human (05) BAA96045
redrmaldnllanlppakpgkssslemtpyntpqlspattpankknrlpiatrsrsrtnmlmdlhmdhegssqetiqevq peevlvislgtgpqltpgmmsenevlnmqlsdggqgdvpvdenklhgkpdktlrfslcsdnlegisegpsnrsnsvssld legesvselgagpsgsngvealqllehegattqdnlddklrkfeirdmmgltddrdisetvsetwstdvlgsdfdpnide drlqeiagaaaenmlgsllclpgsgsvlldpctgstisettseawsvevlpsdseapdlkqeerlqelescsglgstsdd

tdvrevssrpstpglsvvsgisatsedipnkiedlrsecssdfggkdsvtspdmdeithgahqltsppsqsesllamfdp
lsshegasavvrpkvhyarpshpppdppilegavggnearlpnfgshvltpaemeafkqrhsyperlvrsrssdivssvr
rpmsdpswnrrpgneerelppaaaigatslvaaphsssspskdssrgeteerkdsddeksdrnrpwwrkrfvsampkdd
psprlsaqaqvaedildkyrnaikrtspsdgamanyestevmgdgesahdsprdealqnisaddlpdsasqaahpqdsaf
syrdakkklrlalcsadsvafpvlthstrnglpdhtdpedneivcflkvqiaeainlqdknlmaqlqetmrcvcrfdnrt
crkllasiaedyrkrapyiayltrcrqglqttqahlerllqrvlrdkevanryfttvcvrlllesKekkirefiqdfqkl
taaddktaqvedflqflygamaqdviwqnaseeqlqdaqlaiersvmnrifklafypnqdgdilrdqvlhehiqrlskvv
tanhralqipevylreapwpsaqseirtisayktprdkvqcilrmcstimnllslanedsvpgaddfvpvlvfvlikanp
pcllstvqyissfyasclsgeesywwmqftaavefiktiddrk (SEQ ID N):486)

<u>Ydl033cp (6 sequences)</u>

483. Ydl033cp human (01) XP_086901
mqalrhvvcalsggvdsavaalllrrrgyqvtgvfmknwdsldehgvctadkdcedayrvcqildipfhqvsyvkeywn
dvfsdflneyekgrtpnpdivcnkhikfscffhyavdnlgadaiatghyartsledeevfeqkhvkkpeglfrnrfevrna
vkllqaadsfkdqtfflsqvsqdalrrtifplggltkefvkkiaaenrlhhvlqkkesmgmcfigkrnfehfllqylqpr
pghfisiednkvlgthkgwflytlgqranigglrepwyvvekdsvkgdvfvaprtdhpalyrdllrtsrvhwiaeeppaa
lvrdkmmechfrfrhqmalvpcvltlnqdgtvwvtavqavralatgqfavfykgdeclgsgkilrlgpsaytlqkgqrra
gmatespsdspedgpglspll (SEQ ID NO:487)

484. Ydl033cp human (02) O75648
mqalrhvvcalsggvdsavaalllrrrgyqvtgvfmknwdsldehgvctadkdcedayrvcqildipfhqvsyvkeywn
dvfsdflneyekgrtpnpdivcnkhikfscffhyavdnlgadaiatghyartsledeevfeqkhvkkpeglfrnrfevrna
vkllqaadsfkdqtfflsqvsqdalrrtifplggltkefvkkiaaenrlhhvlqkkesmgmcfigkrnfehfllqylqpr
pghfisiednkvlgthkgwflytlgqranigglrepwyvvekdsvkgdvfvaprtdhpalyrdllrtsrvhwiaeeppaa
lvrdkmmechfrfrhqmalvpcvltlnqdgtvwvtavqavralatgqfavfykgdeclgsgkilrlgpsaytlqkgqrra
gmatespsdspedgpglspll (SEQ ID NO:488)

485. Ydl033cp human (03) CAB38414
mqalrhvvcalsggvdsavaalllrrrgyqvtgvfmknwdsldehgvctadkdcedayrvcqildipfhqvsyvkeywn
dvfsdflneyekgrtpnpdivcnkhikfscffhyavdnlgadaiatghyartsledeevfeqkhvkkpeglfrnrfevrna
vkllqaadsfkdqtfflsqvsqdalrrtifplggltkefvkkiaaenrlhhvlqkkesmgmcfigkrnfehfllqylqpr
pghfisiednkvlgthkgwflytlgqranigglrepwyvvekdsvkgdvfvaprtdhpalyrdllrtsrvhwiaeeppaa
lvrdkmmechfrfrhqmalvpcvltlnqdgtvwvtavqavralatgqfavfykgdeclgsgkilrlgpsaytlqkgqrra
gmatespsdspedgpglspll (SEQ ID NO:489)

486. Ydl033cp human (04) CAB63078
mqalrhvvcalsggvdsavaalllrrrgyqvtgvfmknwdsldehgvctadkdcedayrvcqildipfhqvsyvkeywn
dvfsdflneyekgrtpnpdivcnkhikfscffhyavdnlgadaiatghyartsledeevfeqkhvkkpeglfrnrfevrna
vkllqaadsfkdqtfflsqvsqdalrrtifplggltkefvkkiaaenrlhhvlqkkesmgmcfigkrnfehfllqylqpr
pghfisiednkvlgthkgwflytlgqranigglrepwyvvekdsvkgdvfvaprtdhpalyrdllrtsrvhwiaeeppaa
lvrdkmmechfrfrhqmalvpcvltlnqdgtvwvtavqavralatgqfavfykgdeclgsgkilrlgpsaytlqkgqrra
gmatespsdspedgpglspll (SEQ ID NO:490)

487. Ydl033cp human (05) AAL35970

mqalrhvvcalsggvdsavaalllrrrgyqvtgvfmknwdsldehgvctadkdcedayrvcqildipfhqvsyvkeywn
dvfsdflneyekgrtpnpdivcnkhikfscffhyavdnlgadaiatghyartsledeevfeqkhvkkpeglfrnrfevrna
vkllqaadsfkdqtfflsqvsqdalrrtifplggltkefvkkiaaenrlhhvlqkkesmgmcfigkrnfehfllqylqpr
pghfisiednkvlgthkgwflytlgqraniggIrepwyvvekdsvkgdvfvaprtdhpalyrdllrtsrvhwiaeeppaa
lvrdkmmechfrfrhqmalvpcvltlnqdgtvwvtavqavralatgqfavfykgdeclgsgkilrlgpsaytlqkgqrra
gmatespsdspedgpglspll (SEQ ID NO:491)

488. Ydl033cp human (06) AAL38183
mqalrhvvcalsggvdsavaalllrrrgyqvtgvfmknwdsldehgvctadkdcedayrvcqildipfhqvsyvkeywn
dvfsdflneyekgrtpnpdivcnkhikfscffhyavdnlgadaiatghyartsledeevfeqkhvkkpeglfrnrfevrna
vkllqaadsfkdqtfflsqvsqdalrrtifplggltkefvkkiaaenrlhhvlqkkesmgmcfigkrnfehfllqylqpr
pghfisiednkvlgthkgwflytlgqraniggIrepwyvvekdsvkgdvfvaprtdhpalyrdllrtsrvhwiaeeppaa
lvrdkmmechfrfrhqmalvpcvltlnqdgtvwvtavqavralatgqfavfykgdeclgsgkilrlgpsaytlqkgqrra
gmatespsdspedgpglspll (SEQ ID NO:492)

<u>YOR292cp (9 sequences)</u>

489. YOR292cp human (01) AAH16289
hasgrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID NO:493)

490. YOR292cp human (02) NP_002428
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:494)

491. YOR292cp human (03) XP_047175
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:495)

492. YOR292cp human (04) MPV1_HUMAN
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:496)

493. YOR292cp human (05) S45343
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:497)

494. YOR292cp human (06) AAB25210
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:498)

495. YOR292cp human (07) CAA54047
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:499)

496. YOR292cp human (08) 1683146_1
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:500)

497. YOR292cp human (09) AAH01115
malwrayqralaahpwkvqvltagslmglgdiisqqlverrglqehqrgrtltmvslgcgfvgpvvggwykvldrfipgt
tkvdalkkmlldqggfapcflgcflplvgalnglsaqdnwaklqrdypdalitnyylwpavqlanfylvplhyrlavvqc
vaviwnsylswkahrl (SEQ ID No:501)

Appendix B. Functions of host factors

Protein	Function/Phenotype	References
Apl5	Vesicular trafficking	Cowles CR, et al. (1997) The AP-3 adaptor complex is essential for cargo-selective transport to the yeast vacuole. Cell 91(1):109-18.
		Panek HR, et al. (1997) Suppressors of YCK-encoded yeast casein kinase 1 deficiency define the four subunits of a novel clathrin AP-like complex. EMBO J 16(14):4194-204.
		Rous BA, et al. (2002) Role of adaptor complex AP- in targeting wild-type and mutated CD63 to lysosom Mol Biol Cell. 13(3):1071-82.
Ard1	N-terminal acetyltransferase; Nat1p binding	Park EC and Szostak JW (1992) ARD1 and NAT1 proteins form a complex that has N-terminal acetyltransferase activity. EMBO J 11:2087-93
		Polevoda B, et al. (1999) Identification and specificities of N-terminal acetyltransferases from Saccharomyces cerevisiae. EMBO J 18:6155-68
		Lee FJ, et al. (1989) N alpha acetylation is required for normal growth and mating of Saccharomyces cerevisiae. J Bacteriol 171(11):5795-802
		Tribioli,C., Mancini,M., Plassart,E., Bione,S., Rivella,S., Sala,C., Torri,G. and Toniolo,D. Isolation of new genes in distal Xq28: transcriptiona map and identification of a human homologue of the ARD1 N-acetyl transferase of Saccharomyces cerevisiae. Hum. Mol. Genet. 3 (7), 1061-1067 (19
	Transcriptional Silencing	Aparicio OM, et al. (1991) Modifiers of position effect are shared between telomeric and silent mating-type loci in S. cerevisiae. Cell 66:1279-87
	Cell cycle regulation	Whiteway M and Szostak JW (1985) The ARD1 gene of yeast functions in the switch between the mitotic cell cycle and alternative developmental pathways. Cell 43:483-92
Cbc2	Nuclear cap binding protein 2	Fortes P, et al. (1999) Genetic and physical interactions involving the yeast nuclear cap-binding complex. Mol Cell Biol 19(10):6543-53.
		Das B, et al. (2000) The role of nuclear cap binding protein Cbc1p of yeast in mRNA termination and degradation. Mol Cell Biol 20(8):2827-38.

Figure 5

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Cpr7	Cyclophilin D, cyclophilin 40 Sensitivity to Cyclosporin A	Abbas-Terki T, et al. (2001) Hsp104 interacts with hsp90 cochaperones in respiring yeast. Mol Cell Bio 21(22):7569-75 Mayr C, et al. (2000) Cpr6 and cpr7, two closely related Hsp90-associated immunophilins from saccharomyces cerevisiae, differ in their functional properties J Biol Chem 275(44):34140-6 Dolinski K, et al. (1997) All cyclophilins and FK50(binding proteins are, individually and collectively, dispensable for viability in Saccharomyces cerevisiae. Proc Natl Acad Sci U S A 94(24):13093- Duina AA, et al. (1996) Identification of two CyP-4 like cyclophilins in Saccharomyces cerevisiae, one (which is required for normal growth. Yeast 12(10):9 52 Dolinski KJ, Cardenas ME, Heitman J. CNS1 encodes an essential p60/Sti1 homolog in Saccharomyces cerevisiae that suppresses cyclophil 40 mutations and interacts with Hsp90. Mol Cell B 1998 Dec;18(12):7344-52. Bosco DA, et al., Catalysis of cis/trans isomerizatio in native HIV-1 capsid by human cyclophilin A. Pr Natl Acad Sci U S A 2002 Apr 16;99(8):5247-52. Woodfield K, et al. Direct demonstration of a speci interaction between cyclophilin-D and the adenine nucleotide translocase confirms their role in the mitochondrial permeability transition. Biochem J 1 Dec 1;336:287-90 Brenner BG, and Wainberg Z. Heat shock proteins: novel therapeutic tools for HIV-infection? Expert Opin Biol Ther 2001 Jan;1(1):67-77

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Ctk1	Ctk1 kinase	Patturajan M, et al. (1999) Yeast carboxyl-terminal domain kinase I positively and negatively regulates RNA polymerase II carboxyl-terminal domain phosphorylation. J Biol Chem 274(39):27823-8. Hunter T and Plowman GD (1997) The protein kinases of budding yeast: six score and more. Trends Biochem Sci 22(1):18-22 Sterner DE, et al. (1995) The yeast carboxyl-terminal repeat domain kinase CTDK-I is a divergent cyclin-cyclin-dependent kinase complex. Mol Cell Biol 15(10):5716-24 Lee JM and Greenleaf AL (1991) CTD kinase large subunit is encoded by CTK1, a gene required for normal growth of Saccharomyces cerevisiae. Gene Expr 1(2):149-67
Dbf2	Serine/threonine kinase	Liu HY, et al. (1997) DBF2, a cell cycle-regulated protein kinase, is physically and functionally associated with the CCR4 transcriptional regulatory complex. EMBO J 16(17):5289-98. Toyn JH and Johnston LH (1994) The Dbf2 and Dbf20 protein kinases of budding yeast are activated after the metaphase to anaphase cell cycle transition. EMBO J 13(5):1103-13. Johnston LH, et al. (1990) The product of the Saccharomyces cerevisiae cell cycle gene DBF2 has homology with protein kinases and is periodically expressed in the cell cycle. Mol Cell Biol 10(4):1358-66. Millward T, Cron P, Hemmings BA. Molecular cloning and characterization of a conserved nuclear serine(threonine) protein kinase. Proc Natl Acad Sci S A. 1995 May 23;92(11):5022-6. Mah AS, Jang J, Deshaies RJ. Protein kinase Cdc15 activates the Dbf2-Mob1 kinase complex. Proc Natl Acad Sci U S A. 2001 Jun 19;98(13):7325-30.

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Dbp3	RNA helicase, ribosome protein	de la Cruz J, et al. (1999) Unwinding RNA in Saccharomyces cerevisiae: DEAD-box proteins and related families. Trends Biochem Sci 24(5):192-8. Venema J and Tollervey D (1999) Ribosome synthesis in Saccharomyces cerevisiae. Annu Rev Genet 33():261-311. Weaver PL, et al. (1997) Dbp3p, a putative RNA helicase in Saccharomyces cerevisiae, is required for efficient pre-rRNA processing predominantly at site A3. Mol Cell Biol 17(3):1354-65. Chang TH, et al. (1990) Identification of five putative yeast RNA helicase genes. Proc Natl Acad Sci U S A 87(4):1571-5. Lamm,G.M., Nicol,S.M., Fuller-Pace,F.V. and Lamond,A.I. p72: a human nuclear DEAD box protein highly related to p68 Nucleic Acids Res. 24 (19), 3739-3747 (1996).
Dbr1	RNA lariat debranching enzyme	Kim JW, et al. (2000) Human RNA lariat debranching enzyme cDNA complements the phenotypes of Saccharomyces cerevisiae dbr1 and Schizosaccharomyces pombe dbr1 mutants. Nucleic Acids Res 28(18):3666-73. Chapman KB and Boeke JD (1991) Isolation and characterization of the gene encoding yeast debranching enzyme. Cell 65(3):483-92. Nam K, Lee G, Trambley J, Devine SE, Boeke JD. Severe growth defect in a Schizosaccharomyces pon mutant defective in intron lariat degradation. Mol Cell Biol. 1997 Feb;17(2):809-18.
Doa4	Ubiquitin specific protease	Amerik AY, et al. (2000) The Doa4 deubiquitinating enzyme is functionally linked to the vacuolar protei sorting and endocytic pathways. Mol Biol Cell 11(10):3365-80. Amerik AY, et al. (2000) Analysis of the deubiquitinating enzymes of the yeast Saccharomyces cerevisiae. Biol Chem 381(9-10):981-92. Swaminathan S, et al. (1999) The Doa4 deubiquitinating enzyme is required for ubiquitin homeostasis in yeast. Mol Biol Cell 10(8):2583-94. Papa FR and Hochstrasser M (1993) The yeast DOA4 gene encodes a deubiquitinating enzyme related to a product of the human tre-2 oncogene. Nature 366(6453):313-9.

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Elp2	Transcription elongationfactor	Fellows J, et al. (2000) The Elp2 subunit of elongator and elongating RNA polymerase II holoenzyme is a WD40 repeat protein. J Biol Chem 275(17):12896-9. Frohloff F, et al. (2001) Saccharomyces cerevisiae Elongator mutations confer resistance to the Kluyveromyces lactis zymocin. EMBO J 20(8):1993-2003. Winkler GS, Petrakis TG, Ethelberg S, Tokunaga M, Erdjument-Bromage H, Tempst P, Svejstrup JQ. RNA polymerase II elongator holoenzyme is composed of two discrete subcomplexes. J Biol Chem. 2001 Aug 31;276(35):32743-9.
Elp3	Histone acetyltransferase	Frohloff F, et al. (2001) Saccharomyces cerevisiae Elongator mutations confer resistance to the Kluyveromyces lactis zymocin. EMBO J 20(8):1993-2003. Wittschieben BO, et al. (2000) Overlapping roles for the histone acetyltransferase activities of SAGA and elongator in vivo. EMBO J 19(12):3060-8. Sterner DE and Berger SL (2000) Acetylation of histones and transcription-related factors. Microbiol Mol Biol Rev 64(2):435-59. Wittschieben BO, et al. (1999) A novel histone acetyltransferase is an integral subunit of elongating RNA polymerase II holoenzyme. Mol Cell 4(1):123 8. Chinenov Y. A second catalytic domain in the Elp3 histone acetyltransferases: a candidate for histone demethylase activity? Trends Biochem Sci. 2002 Mar;27(3):115-7. Review. Hawkes NA, Otero G, Winkler GS, Marshall N, Dahmus ME, Krappmann D, Scheidereit C, Thomas CL, Schiavo G, Erdjument-Bromage H, Tempst P, Svejstrup JQ. Purification and characterization of the human elongator complex. J Biol Chem. 2002 Jan 25;277(4):3047-52.
Elp4	Transcription elongation factor	Li Y, et al. (2001) A multiprotein complex that interacts with RNA polymerase II elongator. J Biol Chem 276(32):29628-31. Winkler GS, Petrakis TG, Ethelberg S, Tokunaga M Erdjument-Bromage H, Tempst P, Svejstrup JQ. RNA polymerase II elongator holoenzyme is composed of two discrete subcomplexes. J Biol Chem. 2001 Aug 31;276(35):32743-9.
Erv14	Localized to ER-derived vesicles	Vanrheenen SM, et al. (2001) Dsl1p, an essential

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Iki3p (Elp1)	Transcription elongationfactor	Frohloff F, et al. (2001) Saccharomyces cerevisiae Elongator mutations confer resistance to the Kluyveromyces lactis zymocin. EMBO J 20(8):1993-2003. Otero G, et al. (1999) Elongator, a multisubunit component of a novel RNA polymerase II holoenzyme for transcriptional elongation. Mol Cell 3(1):109-18. Yajima H, et al. (1997) Characterization of IKI1 and IKI3 genes conferring pGKL killer sensitivity on Saccharomyces cerevisiae. Biosci Biotechnol Biochem 61(4):704-9
Kcs1	Inositol hexakisphosphate kinase 3	Saiardi A, et al. (2000) The inositol hexakisphospha kinase family. Catalytic flexibility and function in yeast vacuole biogenesis. J Biol Chem 275(32):24686-92. Huang KN and Symington LS (1995) Suppressors o a Saccharomyces cerevisiae pkc1 mutation identify alleles of the phosphatase gene PTC1 and of a novel gene encoding a putative basic leucine zipper protei Genetics 141(4):1275-85. Dubois E, Scherens B, Vierendeels F, Ho MW, Messenguy F, Shears SB. In Saccharomyces cerevisiae, the inositol polyphosphate kinase activit of Kcs1 is required for resistance to salt stress, cell wall integrity and vacuolar morphogenesis. J Biol Chem. 2002 Apr 15 [epub ahead of print] Saiardi A, Caffrey JJ, Snyder SH, Shears S The inositol hexakisphosphate kinase family Catalytic flexibility and function in yeast vacuole biogenesis. J Biol Chem. 2000 Aug 11;275(32):24686-92.
Kti12	Transcription elongationfactor	Frohloff F, et al. (2001) Saccharomyces cerevisiae Elongator mutations confer resistance to the Kluyveromyces lactis zymocin.

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Lsm1	mRNA metabolism; sensitivity to Brefeldin A or monensin	Tharun S and Parker R (2001) Targeting an mRNA for decapping: displacement of translation factors an association of the Lsm1p-7p complex on deadenylated yeast mRNAs. Mol Cell 8(5):1075-83.
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Mad2	Mitotic arrest deficient	Abrieu A, et al. (2001) Mps1 is a kinetochore-associated kinase essential for the vertebrate mitotic checkpoint. Cell 106(1):83-93.
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Nat1	N-terminal acetyltransferase activity; Ard1p binding protein	Park EC and Szostak JW (1992) ARD1 and NAT1 proteins form a complex that has N-terminal acetyltransferase activity. EMBO J 11:2087-93 Polevoda B, et al. (1999) Identification and specificities of N-terminal acetyltransferases from Saccharomyces cerevisiae. EMBO J 18:6155-68 Lee FJ, et al. (1989) N alpha acetylation is required for normal growth and mating of Saccharomyces cerevisiae. J Bacteriol 171(11):5795-802
	Transcriptional Silencing	Aparicio OM, et al. (1991) Modifiers of position effect are shared between telomeric and silent

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Nat3	N-terminal acetyltransferase	Polevoda B, et al. (1999) Identification and specificities of N-terminal acetyltransferases from Saccharomyces cerevisiae. EMBO J 18(21):6155-6ℓ Arnold RJ, et al. (1999) The action of N-terminal acetyltransferases on yeast ribosomal proteins. J Bi(Chem 274(52):37035-40.
Nup84	Nuclear transport protein	Vasu SK and Forbes DJ (2001) Nuclear pores and nuclear assembly. Curr Opin Cell Biol 13(3):363-7: Reynaud A, et al. (2001) Disruption and functional analysis of six ORFs of chromosome IV: YDL103c (QRI1), YDL105w (QRI2), YDL112w (TRM3), YDL113c, YDL116w (NUP84) and YDL167c (NRP1). Yeast 18(3):273-82. Belgareh N, et al. (2001) An evolutionarily conserv NPC subcomplex, which redistributes in part to kinetochores in mammalian cells. J Cell Biol 154(6):1147-60. Stage-Zimmermann T, et al. (2000) Factors affectir nuclear export of the 60S ribosomal subunit In vivc Mol Biol Cell 11(11):3777-89. Bodoor K, Shaikh S, Enarson P, Chowdhury S, Salina D, Raharjo WH, Burke B. Function and assembly of nuclear pore complex proteins. Bioch(Cell Biol. 1999;77(4):321-9. Review. Bastos R, Ribas de Pouplana L, Enarson M, Bodoo K, Burke B. Nup84, a novel nucleoporin that is associated with CAN/Nup214 on the cytoplasmic face of the nuclear pore complex. J Cell Biol. 1997 Jun 2;137(5):989-1000.
Pho23	Transcription factor, Chromatin factor	Loewith R, et al. (2000) Three yeast proteins relate to the human candidate tumor suppressor p33(ING are associated with histone acetyltransferase activities. Mol Cell Biol 20(11):3807-16. Zuniga S, et al. (1999) Disruption of six Saccharomyces cerevisiae novel genes and phenotypic analysis of the deletants. Yeast 15(10B):945-53. Lau WW, et al. (1998) A genetic study of signalin; processes for repression of PHO5 transcription in Saccharomyces cerevisiae. Genetics 150(4):1349-:
Pop2	mRNA metabolism, Transcription	Tucker M, et al. (2001) The Transcription Factor Associated Ccr4 and Caf1 Proteins Are Componen of the Major Cytoplasmic mRNA

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Puf6p	Pumilio homolog	Morris-Desbois C, Rety S, Ferro M, Garin J, Jalinot P. The human protein HSPC021 interacts with Int and is associated with eukaryotic translation initiati factor 3. J Biol Chem. 2001 Dec 7;276(49):45988-9
Rad52	Homologous recombination	Sonoda E, et al. (2001) Homologous DNA recombination in vertebrate cells. Proc Natl Acad S U S A 98(15):8388-94.
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Rpa49	Transcription	Liljelund P, et al. (1992) Characterization and mutagenesis of the gene encoding the A49 subunit RNA polymerase A in Saccharomyces cerevisiae. Proc Natl Acad Sci U S A 89(19):9302-5.
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Rpl14a	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7.

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Rpl16b	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7. Uechi T, Tanaka T, Kenmochi N. A complete map of the human ribosomal protein genes: assignment c 80 genes to the cytogenetic map and implications fo human disorders. Genomics. 2001 Mar 15;72(3):223-30.
Rpl19b	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7. Uechi T, Tanaka T, Kenmochi N. A complete map of the human ribosomal protein genes: assignment c 80 genes to the cytogenetic map and implications fc human disorders. Genomics. 2001 Mar 15;72(3):223-30. Song JM, et al. (1996) Organization and characterization of the two yeast ribosomal protein YL19 genes. Curr Genet 30(4):273-8. Song JM, et al. (1995) Nucleotide sequence and characterization of the Saccharomyces cerevisiae RPL19A gene encoding a homolog of the mammalian ribosomal protein L19. Yeast 11(4):38: 9.
Rpl20b	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7. Uechi T, Tanaka T, Kenmochi N. A complete map of the human ribosomal protein genes: assignment 80 genes to the cytogenetic map and implications f human disorders. Genomics. 2001 Mar 15;72(3):223-30.
Rpl21b	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7. Uechi T, Tanaka T, Kenmochi N. A complete map of the human ribosomal protein genes: assignment 80 genes to the cytogenetic map and implications f human disorders. Genomics. 2001 Mar 15;72(3):223-30.

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Rpl6a	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7.
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Rpp1a	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7.
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Rps10a	Ribosomal protein	Planta RJ and Mager WH (1998) The list of cytoplasmic ribosomal proteins of Saccharomyces cerevisiae. Yeast 14(5):471-7.
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Scp160	mRNA metabolism, control of DNA content	Lang BD and Fridovich-Keil JL (2000) Scp160p, a multiple KH-domain protein, is a component of mRNP complexes in yeast. Nucleic Acids Res 28(7):1576-84.
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Sdf1	Sporulation	Saccharomyces Genome Database (http://genome-

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Sec22	Vesicular trafficking	McNew JA, et al. (2000) Compartmental specificity of cellular membrane fusion encoded in SNARE proteins. Nature 407(6801):153-9.
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Sin3	Recruitment of HDACs; Histone deacetylation; Regulation of transcription	Struhl K (1998) Histone acetylation and transcriptional regulatory mechanisms. Genes Dev 12(5):599-606
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Spt4	Resistance to zymocin	Frohloff F, et al. (2001) Saccharomyces cerevisiae Elongator mutations confer resistance to the Kluyveromyces lactis zymocin. EMBO J 20:1993-2003
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Sse1	Heat shock protein	Mukai H, et al. (1993) Isolation and characterization of SSE1 and SSE2, new members of the yeast HSP7C multigene family. Gene 132(1):57-66. Liu XD, Morano KA, Thiele DJ. The yeast Hsp110 family member, Sse1, is an Hsp90 cochaperone. J Biol Chem. 1999 Sep 17;274(38):26654-60. Storozhenko S, De Pauw P, Kushnir S, Van Montagu M, Inze D. Identification of an Arabidopsis thaliana cDNA encoding a HSP70-related protein belonging t the HSP110/SSE1 subfamily. FEBS Lett. 1996 Jul 15;390(1):113-8. Gurer C. et al., Specific incorporation of heat shock protein 70 family members into primate lentiviral virions. J Virol 2002 May;76(9):4666-70. Brenner BG, and Wainberg Z. Heat shock proteins: novel therapeutic tools for HIV-infection? Expert Opin Biol Ther 2001 Jan;1(1):67-77. Ishihara,K., Yasuda,K. and Hatayama,T. Molecular cloning, expression and localization of human 105 kDa heat shock protein, hsp105. Biochim. Biophys. Acta 1444 (1), 138-142 (1999). Nonoguchi K, Itoh K, Xue JH, Tokuchi H, Nishiyama H, Kaneko Y, Tatsumi K, Okuno H, Tomiwa K and Fujita J. Cloning of human cDNAs for Apg-1 and Apg-2, members of the Hsp110 family, and chromosomal assignment of their genes Gene 237 (1), 21-28 (1999). Fathallah,D.M., Cherif,D., Dellagi,K. and Arnaout,M.A. Molecular cloning of a novel human hsp70 from a B cell line and its assignment to chromosome 5. J. Immunol. 151 (2), 810-813 (1993).
Sto1/Cbc1	Nuclear cap binding protein	Das B, et al. (2000) The role of nuclear cap binding protein Cbc1p of yeast in mRNA termination and degradation. Mol Cell Biol 20(8):2827-38. Zhang D and Rosbash M (1999) Identification of eight proteins that cross-link to pre-mRNA in the yeast commitment complex. Genes Dev 13(5):581- Fortes P, et al. (1999) Genetic and physical interactions involving the yeast nuclear cap-binding

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Figure 5

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Figure 5

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(71) Applicant (*for all designated States except US*): **EMORY UNIVERSITY** [US/US]; 401 Administration Building, Atlanta, GA 30322 (US).

(72) Inventor; and
(75) Inventor/Applicant (*for US only*): **DEVINE, Scott, E.** [US/US]; 1107 Dan Johnson Road, N.E., Atlanta, GA 30307 (US).

(74) Agent: **MEIKLEJOHN, Anita, L.**; Fish & Richardson P.C., 225 Franklin Street, Boston, MA 02110-2804 (US).

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(57) Abstract: Disclosed are compositions and methods that can be used to identify antiviral compounds. The methods can be carried out by exposing a cell that expresses a host factor to a candidate compound. If the expression or activity of the host factor, which is a protein we identified by virtue of its influence on the endogenous retrovirus-like Tyl element in yeast, is inhibited, the candidate compound is a potential antiviral agent. Such agents can be further tested, if desired, by determining whether they inhibit the ability of the virus to infect a cell or replicate within it.

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INTERNATIONAL SEARCH REPORT

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Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X — Y	US 6,242,175 B1 (JACKSON et al.) 05 June 2001 (05.06.2001), Abstract, column 5, lines 42-57, column 6, lines 44-67, column 7, lines 1-20, column 8, lines 1-22, column 9, lines 13-42, column 20, lines 23-65, column 21, lines 25-33, column 22, lines 26-41, column 26, lines 48-67	1-4, 7-13, 15, 17-19, 23 ——— 5, 6, 14, 16, 21, 22
Y	US 5,837,464 A (CAPON et al.) 17 November 1998 (17.11.1998), column 8, lines 44-57, column 26, lines 48-67	5, 6, 14
Y	US 5,230,998 A (NEURATH et al.) 27 July 1993 (27.07.1993) column 24, lines 41-67	16
Y	US 5,578,573 A (HOUGHTEN et al.) 26 November 1996 (26.11.1996) column 4, lines 4-22	20

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